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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:17:16 ; Search time 22.3492 Seconds
(without alignments)
463.411 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	100.0	352	4	US-09-087-232A-13	Sequence 13, Appl
2	1841	100.0	352	4	US-08-861-105-14	Sequence 14, Appl
3	1841	100.0	352	4	US-08-575-967A-2	Sequence 2, Appli
4	1841	100.0	352	4	US-08-833-752-5	Sequence 5, Appli
5	1835	99.7	352	4	US-09-045-583-52	Sequence 52, Appl
6	1835	99.7	352	4	US-09-534-185-52	Sequence 52, Appl
7	1826	99.2	352	3	US-08-466-343D-2	Sequence 2, Appli
8	1814	98.5	352	4	US-09-517-605-5	Sequence 5, Appli
9	1546	84.0	354	4	US-08-724-984A-2	Sequence 2, Appli
10	1364	74.1	347	1	US-08-461-244-3	Sequence 3, Appli
11	1364	74.1	360	1	US-08-450-393A-4	Sequence 4, Appli
12	1364	74.1	360	4	US-08-446-669-4	Sequence 4, Appli
13	1364	74.1	360	4	US-09-045-583-50	Sequence 50, Appl
14	1364	74.1	360	4	US-09-534-185-50	Sequence 50, Appl
15	1364	74.1	360	5	PCT-US95-00476-4	Sequence 4, Appli
16	1350	73.3	360	4	US-08-833-752-7	Sequence 7, Appli
17	1345	73.1	360	4	US-09-045-583-51	Sequence 51, Appl
18	1345	73.1	360	4	US-09-534-185-51	Sequence 51, Appl
19	1224	66.5	344	3	US-08-466-343D-9	Sequence 9, Appli
20	1224	66.5	374	1	US-08-450-393A-2	Sequence 2, Appli
21	1224	66.5	374	4	US-08-446-669-2	Sequence 2, Appli
22	1224	66.5	374	5	PCT-US95-00476-2	Sequence 2, Appli
23	1055	57.3	355	1	US-08-012-988A-2	Sequence 2, Appli
24	1055	57.3	355	1	US-08-450-393A-5	Sequence 5, Appli
25	1055	57.3	355	4	US-08-446-669-5	Sequence 5, Appli
26	1055	57.3	355	4	US-09-239-938-1	Sequence 1, Appli
27	1055	57.3	355	5	PCT-US95-00476-5	Sequence 5, Appli
28	1028	55.8	355	4	US-08-833-752-9	Sequence 9, Appli
29	1009	54.8	355	4	US-09-045-583-53	Sequence 53, Appl
30	1009	54.8	355	4	US-09-534-185-53	Sequence 53, Appl
31	958	52.0	184	4	US-08-833-752-4	Sequence 4, Appli
32	958	52.0	215	4	US-09-087-232A-17	Sequence 17, Appl
33	958	52.0	215	4	US-08-833-752-6	Sequence 6, Appli
34	938.5	51.0	355	4	US-08-575-967A-4	Sequence 4, Appli
35	938.5	51.0	355	4	US-08-847-296B-1	Sequence 1, Appli
36	938.5	51.0	355	4	US-09-045-583-54	Sequence 54, Appl
37	938.5	51.0	355	4	US-09-534-185-54	Sequence 54, Appl
38	919	49.9	360	4	US-08-875-573-20	Sequence 20, Appl
39	919	49.9	360	4	US-09-232-878-2	Sequence 2, Appli
40	919	49.9	360	4	US-09-045-583-55	Sequence 55, Appl
41	919	49.9	360	4	US-09-534-185-55	Sequence 55, Appl
42	899.5	48.9	355	4	US-08-833-752-8	Sequence 8, Appli
43	885	48.1	360	4	US-08-833-752-10	Sequence 10, Appl
44	746.5	40.5	355	1	US-08-461-244-2	Sequence 2, Appli
45	746.5	40.5	355	4	US-09-045-583-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13

Query Match 100.0%; Score 1841; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy         121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db         121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy         181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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RESULT 2
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
;  GENERAL INFORMATION:
;    APPLICANT:  LITTMAN, DAN R.
;    APPLICANT:  DENG, HONGKUI
;    APPLICANT:  ELLMEIER, WILFRIED
;    APPLICANT:  LANDAU, NATHANIEL R.
;    APPLICANT:  LIU, RONG
;    TITLE OF INVENTION:  G-COUPLED RECEPTORS ASSOCIATED WITH
;    TITLE OF INVENTION:  MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
;    TITLE OF INVENTION:  USES THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/861,105
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/666,020
;      FILING DATE:  19-JUN-1996
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/227,319
;      FILING DATE:  13-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-004 N1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-861-105-14
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  Query Match           100.0%;  Score 1841;  DB 4;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-144;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 3
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
;  GENERAL INFORMATION:
;    APPLICANT:  Gray et al.
;    TITLE OF INVENTION:  Chemokine Receptor Materials and Methods
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/575,967A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6265184and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  32918
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-485-1900
;      TELEFAX:  206-485-1662
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
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;     .NAME/KEY:  misc_feature
;      OTHER INFORMATION:  /= "88C amino acid sequence"
US-08-575-967A-2

  Query Match            100.0%;  Score 1841;  DB 4;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-144;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 4
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
;  GENERAL INFORMATION:
;    APPLICANT:  SAMSON, MICHEL
;    APPLICANT:  PARMENTIER, MARC
;    APPLICANT:  VASSART, GILBERT
;    APPLICANT:  LIBERT, FREDERICK
;    TITLE OF INVENTION:  ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;    TITLE OF INVENTION:  AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,752
;      FILING DATE:  9-APR-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-833-752-5

  Query Match            100.0%;  Score 1841;  DB 4;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-144;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 5
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
;  GENERAL INFORMATION:
;    APPLICANT:  Graham, Gerard J. et al.
;    TITLE OF INVENTION:  No. 6287805el Molecules of the G Protein-Coupled
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/045,583
;      FILING DATE:  20-MAR-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MNI-044
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-09-045-583-52

  Query Match            99.7%;  Score 1835;  DB 4;  Length 352;
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  Best Local Similarity   99.4%;  Pred. No. 8.3e-144;
  Matches  350;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 6
US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
;  GENERAL INFORMATION:
;       APPLICANT: Graham, Gerard J. et al.
;       TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
;                           Heptahelical Receptor Superfamily and Uses
;                           Therefor
;       NUMBER OF SEQUENCES: 56
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: LAHIVE & COCKFIELD, LLP
;            STREET: 28 State Street
;            CITY: Boston
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/534,185
;            FILING DATE: 24-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/045,583
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mandragouras, Amy E.
;            REGISTRATION NUMBER: 36,207
;            REFERENCE/DOCKET NUMBER: MNI-044
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)227-7400
;            TELEFAX: (617)742-4214
;   INFORMATION FOR SEQ ID NO: 52:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 352 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

  Query Match             99.7%;  Score 1835;  DB 4;  Length 352;
  Best Local Similarity   99.4%;  Pred. No. 8.3e-144;
  Matches  350;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 7
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
;  GENERAL INFORMATION:
;    APPLICANT:  LI, Yi
;    TITLE OF INVENTION:  POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
;    TITLE OF INVENTION:  CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,343D
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.1150000/EKS/KLM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-466-343D-2

  Query Match             99.2%;  Score 1826;  DB 3;  Length 352;
  Best Local Similarity   98.9%;  Pred. No. 4.6e-143;
  Matches  348;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||:|
Db          1 MDYQVSSPIYDINYYTSEPCPKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCQR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LESMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 8
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
;  APPLICANT: Littman, Dan R.
;  APPLICANT: Kwon, Douglas S.
;  APPLICANT: van Kooyk, Yvette
;  APPLICANT: Geijtenbeck, Tneo
;  TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
;  TITLE OF INVENTION: CELLS
;  FILE REFERENCE: 1049-1-017
;  CURRENT APPLICATION NUMBER: US/09/517,605
;  CURRENT FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-517-605-5

  Query Match             98.5%;  Score 1814;  DB 4;  Length 352;
  Best Local Similarity   98.3%;  Pred. No. 4.5e-142;
  Matches  346;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:| |||||||||||||||||||||||||||||||||||:||||||
Db          1 MDYQVSSPTYDIDYDTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILVLINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 9
US-08-724-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
;  GENERAL INFORMATION:
;    APPLICANT:  Derk Bergsma, Mary Brawner, and Usman Shabon
;    TITLE OF INVENTION:  No. 6388055el Mouse Genomic Clone of the CC-
;    TITLE OF INVENTION:  CKR5 Receptor
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road, P.O. Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM 486
;      OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;      SOFTWARE:  MICROSOFT WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,984A
;      FILING DATE:  October 3, 1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William T. Han
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  ATG50023
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610 270 5024
;      TELEFAX:  610 270 5090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  354
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-724-984A-2

  Query Match             84.0%;  Score 1546;  DB 4;  Length 354;
  Best Local Similarity   81.4%;  Pred. No. 5.1e-120;
  Matches  288;  Conservative   29;  Mismatches   35;  Indels    2;  Gaps    1;

Qy          1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC 58
              ||:| | |  ||||:|  | ||||||||||||:|||||||||||||| |||:| ||||:|
Db          1 MDFQGSVPTYIYDIDYGMSAPCQKINVKQIAAQLLPPLYSLVFIFGFAGNMMVFLILISC 60

Qy         59 KRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF 118
              |:|||:|||||||||||| ||||:|||||||| :| ||| ||:: ||:| ||:| ||||
Db         61 KKLKSVTDIYLLNLAISDLLFLLTLPFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFF 120

Qy        119 IILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTC 178
              ||||||||||:|||||||  || |||:|||:|||||||||| |||||||||  ||||
Db        121 IILLTIDRYLAIVHAVFALKVTTVNFGVITSVVTWVVAVFASLPEIIFTRSQKEGFHYTC 180

Qy        179 SSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIF 238
              | |||:|| |||:|||||:||| |:||||||:|||||| || ||||||||||||||||
Db        181 SPHFPHTQYHFWKSFQTLKMVILSLILPLLVMIICYSGILHTLFRCRNEKKRHRAVRLIF 240

Qy        239 TIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYA 298
                |||||||| |||||||| ||||||||||||||||||||| ||||||||||:||:|||
Db        241 AIMIVYFLFWTPYNIVLLLTTFQEFFGLNNCSSSNRLDQAMQATETLGMTHCCLNPVIYA 300

Qy        299 FVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||:|| |||:||| ||||| |||||: |:| |||||||||| |:| ||
Db        301 FVGEKFRSYLSVFFRKHIVKRFCKRCSIFQQDNPDRVSSVYTRSTGEHEVSTGL 354
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RESULT 10
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
;  GENERAL INFORMATION:
;    APPLICANT:  Soppet, Daniel R.
;    APPLICANT:  Yi, Li
;    APPLICANT:  Ruben, Steven M.
;    APPLICANT:  Rosen, Craig A.
;    TITLE OF INVENTION:  HUMAN G-PROTEIN RECEPTOR HGBER32
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;      ADDRESSEE:  STUART & OLSTEIN
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,244
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-445
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  347 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-244-3

  Query Match             74.1%;  Score 1364;  DB 1;  Length 347;
  Best Local Similarity   75.5%;  Pred. No. 4.7e-105;
  Matches  259;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    2;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||:|||||||:|| :|||||
Db         11 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 68

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db         69 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 128

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||||:||||||:||||||: |||   | |  :||    :
Db        129 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 184

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   |||||||||:||||||||||||||||||||||||:||||||||||
Db        185 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 244

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
              |||||:||||||||||:|| |:::|||| |||||||||||||||||||||||| ||
Db        245 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 304

Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||:||| ||||| | :| :|  :  :|  | ||||||:| ||
Db        305 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 347


RESULT 11
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,393A
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5165
;      TELEFAX:  415-8857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-450-393A-4

  Query Match             74.1%;  Score 1364;  DB 1;  Length 360;
  Best Local Similarity   75.5%;  Pred. No. 4.9e-105;
  Matches  259;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    2;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||||:||||||:||||||: |||   | |  :||    :
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   |||||||||:||||||||||||||||||||||||:||||||||||
Db        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
              |||||:||||||||||:|| |:::|||| |||||||||||||||||||||||| ||
Db        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317

Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||:||| ||||| | :| :|  :  :|  | ||||||:| ||
Db        318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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```
RESULT 12
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,669
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Neeley, Richard
;      REGISTRATION NUMBER:  30,092
;      REFERENCE/DOCKET NUMBER:  UCAL-237/01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5000
;      TELEFAX:  415-857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-446-669-4

  Query Match             74.1%;  Score 1364;  DB 4;  Length 360;
  Best Local Similarity   75.5%;  Pred. No. 4.9e-105;
  Matches  259;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    2;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||||:||||||:||||||: |||   | |  :||   :
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   |||||||||:|||||||||||||||||||||||||:||||||||||
Db        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
              |||||:||||||||||:|| |:::|||| ||||||||||||||||||||||||| ||
Db        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317

Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||:||| ||||| | :| :|  :  :|  | ||||||:| ||
Db        318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360


RESULT 13
US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
;  GENERAL INFORMATION:
;    APPLICANT:  Graham, Gerard J. et al.
;    TITLE OF INVENTION:  No. 6287805el Molecules of the G Protein-Coupled
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/045,583
;      FILING DATE:  20-MAR-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MNI-044
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-09-045-583-50

  Query Match             74.1%;  Score 1364;  DB 4;  Length 360;
  Best Local Similarity   75.5%;  Pred. No. 4.9e-105;
  Matches  259;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    2;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||||:||||||:||||||: |||   | |  :||   :
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   |||||||||:|||||||||||||||||||||||||:||||||||||
Db        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
              |||||:||||||||||:|| |:::|||| ||||||||||||||||||||||||| ||
Db        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317

Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||:||| ||||| | :| :|  :  :|  | ||||||:| ||
Db        318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360


RESULT 14
US-09-534-185-50
; Sequence 50, Application US/09534185
```

```
; Patent No. 6403767
;   GENERAL INFORMATION:
;        APPLICANT: Graham, Gerard J. et al.
;        TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
;                            Heptahelical Receptor Superfamily and Uses
;                            Therefor
;        NUMBER OF SEQUENCES: 56
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD, LLP
;             STREET: 28 State Street
;             CITY: Boston
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/534,185
;             FILING DATE: 24-Mar-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/045,583
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mandragouras, Amy E.
;             REGISTRATION NUMBER: 36,207
;             REFERENCE/DOCKET NUMBER: MNI-044
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)227-7400
;             TELEFAX: (617)742-4214
;   INFORMATION FOR SEQ ID NO: 50:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 360 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

  Query Match             74.1%;  Score 1364;  DB 4;  Length 360;
  Best Local Similarity   75.5%;  Pred. No. 4.9e-105;
  Matches  259;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    2;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
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Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||:||||||:||||||: |||   | |  :||    :
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   ||||||||:|||||||||||||||||||||||||:||||||||||||
Db        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
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Db        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317

Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||:||| ||||| | :| :|  :  :|  | |||||||:| ||
Db        318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360


RESULT 15
PCT-US95-00476-4
;  Sequence 4, Application PC/TUS9500476
;   GENERAL INFORMATION:
;     APPLICANT:  The Regents of the University of California
;     TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;     TITLE OF INVENTION:  PROTEIN RECEPTORS
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Robbins, Berliner & Carson
;       STREET:  201 N. Figueroa Street, 5th Floor
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  90012-2628
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/00476
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Berliner, Robert
;       REGISTRATION NUMBER:  20,121
;       REFERENCE/DOCKET NUMBER:  5555-291
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  310-977-1001
;       TELEFAX:  310-977-1003
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  360 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-00476-4

  Query Match             74.1%;  Score 1364;  DB 5;  Length 360;
  Best Local Similarity   75.5%;  Pred. No. 4.9e-105;
  Matches  259;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    2;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
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Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||:||||||:||||||: |||   | |  :||    :
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   ||||||||:|||||||||||||||||||||||||:||||||||||||
Db        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
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Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||:||| ||||| | :| :|  :  :|  | |||||||:| ||
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Search completed: June  3, 2003, 15:23:37
Job time : 37.3492 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:09:10 ; Search time 64.5644 Seconds
(without alignments)
726.472 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	100.0	352	18	AAW27407	Human CCR5. Homo
2	1841	100.0	352	18	AAW27123	Human chemokine re
3	1841	100.0	352	19	AAW23835	Human CC chemokine
4	1841	100.0	352	20	AAW88232	HIV-1 co-receptor
5	1841	100.0	352	22	AAG80111	Human CCR5 protein
6	1841	100.0	352	22	AAB82948	Human HIV-1 co-rec
7	1841	100.0	352	22	AAB83354	Human CCR5 protein
8	1841	100.0	352	22	AAE04321	Human chemokine re
9	1841	100.0	352	23	ABB08343	Human chemokine (C
10	1841	100.0	352	23	AAM52828	Human CC chemokine
11	1841	100.0	439	20	AAY41280	Fusion protein con
12	1836	99.7	371	19	AAW23834	Human CC chemokine
13	1835	99.7	352	22	ABB56342	Non-endogenous hum
14	1835	99.7	352	23	AAM52829	Human CCR5 Gln 55
15	1833	99.6	352	22	AAE07039	Human G-protein ch
16	1833	99.6	352	22	AAE07048	Human G-protein ch
17	1833	99.6	352	22	AAB46858	Human HDGNR10 prot
18	1833	99.6	352	23	AAU97152	Human G-protein ch
19	1826	99.2	352	18	AAW07602	Human G-protein ch
20	1826	99.2	352	21	AAY80128	Human G-protein ch
21	1826	99.2	352	22	AAE07037	Human G-protein ch
22	1826	99.2	352	22	AAE07046	Human G-protein ch
23	1826	99.2	352	23	AAU97150	Human G-protein ch
24	1814	98.5	352	22	AAG79089	Amino acid sequenc
25	1807	98.2	352	18	AAW27125	Macaque chemokine
26	1641.5	89.2	332	18	AAW26766	Human chemokine re
27	1546	84.0	354	19	AAW54037	Mouse CC-CKR5 prot
28	1365	74.1	360	22	AAU07613	Human CCR2-64I pol
29	1364	74.1	360	16	AAR79166	Human monocyte che
30	1364	74.1	360	18	AAW35833	Human monocyte che
31	1364	74.1	360	22	AAG80108	Human CCR2b protei
32	1364	74.1	360	22	AAU07614	Human wild-type CC
33	1358	73.8	360	22	ABB56340	Non-endogenous hum
34	1224	66.5	374	16	AAR79165	Human monocyte che
35	1224	66.5	374	22	AAG80107	Human CCR2a protei
36	1138.5	61.8	329	22	AAB46859	Human MCP-1 recept
37	1055	57.3	355	15	AAR52749	C-C chemokine rece
38	1055	57.3	355	18	AAW26588	Human MIP-1 alpha/
39	1055	57.3	355	18	AAW25751	Human MIP-1alpha/R
40	1055	57.3	355	21	AAB20571	Human CC-chemokine
41	1016.5	55.2	355	18	AAW29179	Rat CC chemokine r
42	958	52.0	184	18	AAW27406	Inactive human CCR
43	958	52.0	215	18	AAW27408	Inactive human CCR
44	958	52.0	215	20	AAW88238	HIV-1 co-receptor
45	942.5	51.2	355	19	AAW51744	Human C-C chemokin

ALIGNMENTS

RESULT 1
AAW27407
ID AAW27407 standard; Protein; 352 AA.
XX
AC AAW27407;
XX
DT 14-APR-1998 (first entry)
XX
DE Human CCR5.
XX
KW Human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder.
XX
OS Homo sapiens.
XX
PN WO9732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE00023.
XX
PR 06-AUG-1996; 96EP-0870102.
PR 01-MAR-1996; 96EP-0870021.
XX
PA (EURO-) EUROSCREEN SA.
XX
PI Libert F, Parmentier M, Samson M, Vassart G;
XX
DR WPI; 1997-479829/44.

```
DR   N-PSDB; AAT90117.
XX
PT   Active and inactive forms of human CC chemokine receptor CCR-5 -
PT   useful to diagnose, prevent and/or treat inflammatory disorders,
PT   autoimmune disease and viral infection
XX
PS   Claim 4; Fig 1b-c; 94pp; English.
XX
CC   The present sequence is human CC (Cys-Cys) chemokine receptor
CC   5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES
CC   chemokines, but not by monocyte chemoattractant protein 1 (MCP-1),
CC   MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product
CC   alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of
CC   human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2).
CC   CCR5 or its cDNA can used to diagnose, treat and/or prevent
CC   inflammatory diseases, e.g. rheumatoid arthritis,
CC   glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC   psoriasis, viral infections, especially HIV-1 or HIV-2 infection,
CC   cancer, atherosclerosis and autoimmune disorders.
XX
SQ   Sequence   352 AA;

  Query Match             100.0%;  Score 1841;  DB 18;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 2
AAW27123
ID   AAW27123 standard; Protein; 352 AA.
XX
AC   AAW27123;
XX
DT   14-DEC-1997  (first entry)
XX
DE   Human chemokine receptor 88C.
XX
KW   Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
KW   tumour; asthma; viral infection; AIDS; inflammation;
KW   autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW   G protein coupled receptor; ligand; modulator; antibody; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..32
FT                   /label= Extracellular_domain
FT   Domain          56..67
FT                   /label= Intracellular_domain
FT   Domain          89..112
FT                   /label= Extracellular_domain
FT   Domain          125..145
FT                   /label= Intracellular_domain
FT   Domain          166..191
FT                   /label= Extracellular_domain
FT   Domain          213..235
FT                   /label= Intracellular_domain
FT   Domain          259..280
FT                   /label= Extracellular_domain
FT   Domain          301..352
FT                   /label= Intracellular_domain
XX
PN   WO9722698-A2.
XX
PD   26-JUN-1997.
XX
PF   20-DEC-1996;   96WO-US20759.
XX
PR   07-JUN-1996;   96US-0661393.
PR   20-DEC-1995;   95US-0575967.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Gray PW,  Raport CJ,  Schweickart VL;
XX
DR   WPI; 1997-341689/31.
DR   N-PSDB; AAT85161.
XX
PT   New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT   to modulate leukocyte trafficking, e.g. for treatment of
PT   inflammation, tumours, viral infections, autoimmune diseases, etc.
XX
PS   Claim 16; Page 47-48; 65pp; English.
XX
CC   This polypeptide sequence comprises novel human chemokine receptor
CC   88C, a G protein coupled receptor that is involved in leukocyte
CC   trafficking.  Its amino sequence was deduced from a cDNA clone
CC   (AAT85161) isolated from a macrophage library.  It shows 62% identity
CC   to CCCKR1.  Chemokine receptor 88-2B (see AAW27124) has also been
CC   identified.  88C and 88-2B receptors and their polypeptide fragments
CC   can be produced in transformed host cells.  The receptors, peptides
CC   comprising one or more of the extracellular or intracellular
CC   domains, and anti-receptor antibodies can be used to modulate
CC   receptor activities, particularly ligand and G protein binding, and
CC   are potentially potentially useful in the treatment of
CC   atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC   infection, AIDS, inflammatory conditions, pathological immune
CC   response, abnormal haematopoietic processes etc.
XX
SQ   Sequence   352 AA;

  Query Match             100.0%;  Score 1841;  DB 18;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 3
AAW23835
ID   AAW23835 standard; Protein; 352 AA.
XX
AC   AAW23835;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Human CC chemokine receptor 5 (CCR5).
XX
KW   CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW   human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW   transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          29..55
FT                   /label= I
FT                   /note= "transmembrane domain"
FT   Region          109..120
FT                   /note= "extracellular loop-1 (Claim 19)"
FT   Domain          104..126
FT                   /label= III
FT                   /note= "transmembrane domain"
FT   Domain          143..171
FT                   /label= IV
FT                   /note= "transmembrane domain"
FT   Region          187..210
FT                   /note= "extracellular loop-2 (Claim 19)"
FT   Domain          194..219
FT                   /label= V
FT                   /note= "transmembrane domain"
FT   Domain          238..258
FT                   /label= VI
FT                   /note= "transmembrane domain"
FT   Region          261..276
FT                   /note= "extracellular loop-3 (Claim 19)"
FT   Domain          277..300
FT                   /label= VII
FT                   /note= "transmembrane domain"
XX
PN   WO9745543-A2.
XX
PD   04-DEC-1997.
XX
PF   28-MAY-1997;   97WO-US09586.
XX
PR   28-MAY-1996;   96US-0018508.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Alkhatib G,  Berger EA,  Broder CC,  Combadiere C;
PI   Feng Y,  Kennedy PE, Murphy PM;
XX
DR   WPI; 1998-032650/03.
DR   N-PSDB; AAT76920.
XX
PT   CC chemokine receptor 5 polypeptide - used to inhibit membrane
PT   fusion between HIV and a target cell
XX
PS   Claim 68; Fig 1C; 70pp; English.
XX
CC   This protein sequence comprises of a novel human macrophage-selective
CC   CC chemokine receptor that has been designated CCR5.  The sequence
CC   was deduced from an isolated cDNA clone (see AAT76920).  An Ala127Leu
CC   variant (see W238340 of CCR5 was also identified.  The susceptibility
CC   of human macrophages to HIV infection depends on cell surface
CC   expression of CD4 and CCR5.  CCR5 is a member of the 7-transmembrane
CC   superfamily of G-protein coupled cell surface molecules.  It plays
CC   an essential role in the membrane fusion step of infection by some
CC   HIV isolates.  The establishment of stable, non-human cell lines
CC   and transgenic mammals having cells that coexpress human CD4 and
CC   CCR5 provides valuable tools for research of HIV infection.
CC   Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
CC   agents capable of blocking membrane fusion between HIV and target
CC   cells represent potential anti-HIV therapeutics for macrophage
CC   tropic strains of HIV.
XX
SQ   Sequence   352 AA;

  Query Match            100.0%;  Score 1841;  DB 19;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 4
AAW88232
ID   AAW88232 standard; Protein; 352 AA.
XX
AC   AAW88232;
XX
DT   15-MAR-1999  (first entry)
XX
DE   HIV-1 co-receptor CCR5.
XX
KW   HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
KW   gene therapy; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          32..56
FT                   /note= "transmembrane domain 1"
FT   Domain          67..87
FT                   /note= "transmembrane domain 2"
FT   Misc-difference 101
FT                   /note= "corresponds to TGT (Cys) in wild-type CCR5,
FT                    TGA (Stop) in CCr5m303"
FT   Domain          103..124
FT                   /note= "transmembrane domain 3"
FT   Domain          142..167
FT                   /note= "transmembrane domain 4"
FT   Domain          200..223
```

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FT                   /note= "transmembrane domain 5"
FT   Domain          236..260
FT                   /note= "transmembrane domain 6"
FT   Domain          275..301
FT                   /note= "transmembrane domain 7"
XX
PN   WO9854317-A1.
XX
PD   03-DEC-1998.
XX
PF   29-MAY-1998;    98WO-EP03437.
XX
PR   30-MAY-1997;    97US-0048057.
XX
PA   (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
PI   Arenzana Siesdedos F,  Beretta A,  Braun J,  Quillent C;
XX
DR   WPI; 1999-059835/05.
DR   N-PSDB; AAV84126.
XX
PT   New CCR5 variant protein of the HIV-1 co-receptor - useful in
PT   developing resistance of CCR5-expressing cells to HIV-1 infection
XX
PS   Disclosure; Page 34-35; 55pp; English.
XX
CC   This is the amino acid sequence of wild-type human CCR5, which
CC   serves as a co-receptor for infection by macrophage-tropic
CC   (M-tropic) strains of HIV-1.  The invention relates to the
CC   identification of a CCR5 variant (see AAW88231), designated CCR5m303,
CC   comprising the first two transmembrane domains of wild-type CCR5,
CC   but lacking transmembrane domains 3-7.  The presence of the
CC   CCR5m303 variant with the wild type CCR5 allele shows a positive
CC   correlation with resistance to infection with M-tropic HIV-1
CC   strains, and may indicate slower progression of the disease.  The
CC   detection of CCR5 variants may be used to identify individuals at
CC   lower risk of infection relative to the general population who, if
CC   infected, may exhibit slower progression to AIDS.  Probes and
CC   primers (see AAV84127-36) are provided for use in diagnostic methods
CC   for detecting the presence of such variants.  A method is provided
CC   for inhibiting HIV-1 infection of a cell expressing the CCR5
CC   receptor.  This involves introducing a nucleic acid encoding a CCR5
CC   variant into the cell, thereby reducing the number of functional
CC   CCR5 molecules present on the cell surface.
XX
SQ   Sequence   352 AA;

  Query Match            100.0%;  Score 1841;  DB 20;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 5
AAG80111
ID   AAG80111 standard; Protein; 352 AA.
XX
AC   AAG80111;
XX
DT   17-JAN-2002  (first entry)
XX
DE   Human CCR5 protein.
XX
KW   Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW   inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW   chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW   antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW   antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO200172830-A2.
XX
PD   04-OCT-2001.
XX
PF   02-APR-2001; 2001WO-EP03708.
XX
PR   31-MAR-2000; 2000DE-1016013.
XX
PA   (IPFP-) IPF PHARM GMBH.
PA   (FORS/) FORSSMANN U.
XX
PI   Forssmann W,  Adermann K,  Heitland A,  Spodsberg N;
XX
DR   WPI; 2001-626256/72.
XX
PT   Diagnostic agent containing two or more receptor-specific ligands,
PT   useful for detecting tumors, inflammation etc., also therapeutic use of
PT   ligand inhibitors -
XX
PS   Disclosure; Page 10; 26pp; German.
XX
CC   This invention describes a novel diagnostic agent (A) comprising at least
CC   two different ligands (I) for receptors (II) that are implicated in
CC   disease. (A) are used for the diagnosis of tumors (especially colorectal
CC   or prostatic), organ rejection, inflammation and autoimmune diseases.
CC   Also inhibitors of (I) are used therapeutically against tumors (and their
CC   metastases), inflammation (particularly bronchial asthma or chronic bowel
CC   inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC   where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC   endocrine, motor or urogenital systems or skin are affected, and bone
CC   marrow diseases. The products of the invention are chemokine derivatives
CC   which have cytostatic, antiinflammatory, antiasthmatic,
CC   immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC   Chemokines act on specific tumor and inflammatory cells through a
CC   constellation of chemokine receptors (CR), which control migration and
CC   proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC   fragments used to illustrate the method of the invention.
XX
SQ   Sequence   352 AA;

  Query Match            100.0%;  Score 1841;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
```

```
Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 6
AAB82948
ID   AAB82948 standard; Protein; 352 AA.
XX
AC   AAB82948;
XX
DT   21-DEC-2001  (first entry)
XX
DE   Human HIV-1 co-receptor CCR5.
XX
KW   CCR5; chemokine; co-receptor; human immunodeficiency virus type 1;
KW   HIV-1; infection; therapy; vaccine; anti-HIV-1.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    2..18
FT                   /note= "binds to HIV-1 gp120"
XX
PN   WO200164710-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06699.
XX
PR   29-FEB-2000; 2000US-185667P.
PR   19-MAY-2000; 2000US-205839P.
PR   07-FEB-2001; 2001US-267231P.
XX
PA   (PROG-) PROGENICS PHARM INC.
PA   (AARO-) AARON DIAMOND AIDS RES CENT.
XX
PI   Dragic T,  Olson WC;
XX
DR   WPI; 2001-611273/70.
DR   N-PSDB; AAH26903.
XX
PT   Novel compounds comprising specific amino acids within CCR5 (HIV 1
PT   co-receptor) amino terminal domain including negatively charged and two
PT   sulfated tyrosine residues is useful for treating HIV infection in
PT   humans
XX
PS   Claim 1; Page 30; 163pp; English.
XX
CC   The present sequence is that of human HIV-1 co-receptor CCR5.
CC   Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1
CC   gp120-binding site that determines the specificity of the
CC   interaction between CCR5 and HIV-1 gp120.  Post-translational
CC   sulfation of the tyrosine residues in the CCR5 N-terminus is
CC   required for gp120 binding and may critically modulate the
CC   susceptibility of target cells to HIV-1 infection in vivo.  The
CC   invention provides claimed sulfated peptides (see AAB82947) that
CC   are based on the CCR5 N-terminal region and which are effective
CC   for inhibiting HIV-1 binding to CCR5.  These peptides are used in
CC   claimed methods of inhibiting HIV infection of CD4+ cells, of
CC   preventing CD4+ cells from becoming infected with HIV, of treating
CC   a subject whose CD4+ cells are infected with HIV, and of
CC   identifying an agent which inhibits binding of a CCR5 ligand to a
CC   CCR5 receptor.  The methods may be carried out in a subject,
CC   especially a human, infected (therapeutic method), not infected
CC   with HIV (prophylactic method), or in a subject who is not infected
CC   with, but has been exposed to, HIV.
XX
SQ   Sequence   352 AA;

  Query Match           100.0%;  Score 1841;  DB 22;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 7
AAB83354
ID   AAB83354 standard; Protein; 352 AA.
XX
AC   AAB83354;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human CCR5 protein sequence.
XX
KW   Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
KW   human immunodeficiency virus; anti-inflammatory disease; human.
XX
OS   Homo sapiens.
XX
PN   EP1118858-A2.
XX
PD   25-JUL-2001.
XX
PF   03-JAN-2001; 2001EP-0300020.
XX
PR   12-JAN-2000; 2000GB-0000659.
PR   12-JAN-2000; 2000GB-0000661.
PR   12-JAN-2000; 2000GB-0000663.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Dobbs S,  Perros M,  Rickett GA;
XX
DR   WPI; 2001-477088/52.
DR   N-PSDB; AAF87099.
XX
PT   Determining if an agent can modulate CCR5-gp120 interaction, comprises
PT   incubating the agent with CCR5 and gp120 and determining if the agent
```

```
PT   modulates the interaction -
XX
PS   Claim 1; Page 110; 113pp; English.
XX
CC   This sequence represents the human CCR5 protein sequence.
CC   The invention relates to a method for determining whether an agent is
CC   capable of modulating the interaction of chemotactic chemokine receptor 5
CC   (CCR5) with gp120, comprising incubating the agent with CCR5 and gp120
CC   and determining whether the agent modulates the interaction, where gp120
CC   is associated with CD4, and where the interaction is a low affinity
CC   binding. The method is used to identify an agent capable of modulating
CC   the interaction of CCR5 with gp120. An agent identified by the method
CC   is used to prepare a pharmaceutical composition for the treatment of a
CC   disease or condition associated with CCR5 and gp120 interaction, to treat
CC   a subject with a disease or condition associated with CCR5 and gp120
CC   interaction, and for preparing a pharmaceutical for treating human
CC   immunodeficiency virus (HIV). It can also be treat anti-inflammatory
CC   diseases. The method is commercially useful, amenable to high throughput
CC   screening, and detects interaction of gp120 with cells expressing only
CC   CCR5.
XX
SQ   Sequence   352 AA;

  Query Match             100.0%;  Score 1841;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 8
AAE04321
ID   AAE04321 standard; Protein; 352 AA.
XX
AC   AAE04321;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
XX
KW   Human; transformed mammalian cell; CD4; reporter gene; translocation;
KW   human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
KW   chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
KW   CC-CKR-5; envelope glycoprotein; anti-HIV.
XX
OS   Homo sapiens.
XX
PN   US6258527-B1.
XX
PD   10-JUL-2001.
XX
PF   21-MAY-1997;   97US-0861105.
XX
PR   20-MAY-1996;   96US-0017157.
PR   19-JUN-1996;   96US-0020043.
PR   19-MAY-1997;   97US-0858660.
XX
PA   (AARO-) AARON DIAMOND AIDS RES CENT.
PA   (UYNY ) UNIV NEW YORK STATE.
XX
PI   Littman DR,  Deng H,  Ellmeier W,  Landau NR,  Liu R;
XX
DR   WPI; 2001-417127/44.
DR   N-PSDB; AAD08577.
XX
PT   Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
PT   and HIV LTR for identification of drugs and antibodies for treatment of
PT   HIV -
XX
PS   Disclosure; Column 47-50; 37pp; English.
XX
CC   The present invention relates to a transformed mammalian cell that
CC   contains a gene encoding CD4, a construct encoding a reporter gene under
CC   the regulation of an human immuno deficiency virus (HIV) long terminal
CC   repeat (LTR) and that has been transduced with a vector encoding a
CC   human chemokine receptor (CKR) where the CD4 and the CKR are present on
CC   the cell surface of transformed mammalian cell. The invention is useful
CC   for identifying drugs or antibodies that interfere with the
CC   translocation of HIV into transformed mammalian cell or for identifying
CC   a human chemokine receptor that facilitates the infection of a
CC   particular HIV strain into the transformed mammalian cell. Compounds
CC   identified can be used to treat cellular dysfunction and to prevent or
CC   combat HIV infection. The present sequence is a human chemokine receptor
CC   (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for
CC   entry mediated by the envelope glycoproteins of primary macrophage-tropic
CC   strains of HIV-1.
XX
SQ   Sequence   352 AA;

  Query Match             100.0%;  Score 1841;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-200;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 9
ABB08343
ID   ABB08343 standard; Protein; 352 AA.
XX
AC   ABB08343;
XX
```

DT 18-JUN-2002 (first entry)
XX
DE Human chemokine (C-C motif) receptor 5 polypeptide.
XX
KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
KW chromosome 3p21.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 55
FT /label= Leu, Gln
FT Misc-difference 182
FT /label= Phe, Leu
FT Misc-difference 223
FT /label= Arg, Gln
XX
PN WO200177125-A2.
XX
PD 18-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10708.
XX
PR 05-APR-2000; 2000US-194361P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kliem SE, Koshy B;
XX
DR WPI; 2002-041282/05.
DR N-PSDB; ABA97318, ABA97319.
XX
PT New haplotypes of the human chemokine (C-C motif) receptor 5 gene,
PT useful to diagnose and treat diseases associated with its abnormal
PT expression or function, including human immunodeficiency virus-1
PT infection -
XX
PS Claim 29; Fig 3; 61pp; English.
XX
CC The present sequence is that of a polypeptide encoded by the human
CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
CC ABA97318, ABA97319). The specification describes haplotyping the CCR5
CC gene of an individual by determining if the individual has one of the
CC CCR5 haplotypes or haplotype pairs fully defined in the specification.
CC The specification also describes an isolated polynucleotide comprising a
CC nucleotide sequence which is a polymorphic variant of the reference CCR5
CC gene sequence and comprises an isogene defined by a haplotype described
CC in the specification and its encoded polypeptide. The methods of the
CC invention are useful to diagnose and develop treatment for diseases
CC associated with abnormal expression or function of the gene. The CCR5
CC isogenes and the screened compounds are useful for treating human
CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
CC immunodeficiency syndrome (AIDS). The invention has antiviral
CC applications. The specification describes genotyping the CCR5 gene of an
CC individual; predicting a haplotype pair for the CCR5 gene of an
CC individual; identifying an association between a trait and a haplotype or
CC haplotype pair of the CCR5 gene. The specification describes a
CC composition comprising a genotyping oligonucleotide for detecting a CCR5
CC polymorphism; a recombinant non-human organism transformed with CCR5
CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
CC an isolated antibody specific for the CCR5 polypeptide and a method for
CC screening drugs targeting the CCR5 polypeptide.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 1841; DB 23; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-200;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
```

RESULT 10
AAM52828
ID AAM52828 standard; Protein; 352 AA.
XX
AC AAM52828;
XX
DT 22-FEB-2002 (first entry)
XX
DE Human CC chemokine receptor 5 (CCR5).
XX
KW CCR5; CC chemokine receptor 5; human; HIV infection;
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW drug screening; identification.
XX
OS Homo sapiens.
XX
PN WO200171346-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09155.
XX
PR 21-MAR-2000; 2000US-190946P.
PR 21-MAR-2000; 2000US-190996P.
PR 21-MAR-2000; 2000US-191299P.
PR 20-MAR-2001; 2001US-0813448.
PR 20-MAR-2001; 2001US-0813651.
PR 20-MAR-2001; 2001US-0813653.
XX
PA (CONS-) CONSENSUS PHARM INC.
XX
PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX
DR WPI; 2002-010610/01.
DR N-PSDB; ABA02317.
XX
PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
PT comprises binding a molecule from library to a molecule having binding
PT property corresponding to CCR5 and identifying bound molecule -
XX
PS Example 3; Fig 4A; 50pp; English.
XX
CC The invention relates to a method for identifying a binding compound
CC for CC chemokine receptor 5 (CCR5). The method involves screening a
CC library of test molecules (particularly peptides) with immobilised CCR5,
CC and then identifying those molecules which bind. The invention also
CC relates to CCR5-binding molecules identified using the method of the
CC invention, methods for identifying consensus motifs for CCR5-binding
CC peptides, a transfer vector encoding tagged CCR5, a computer-aided

CC methods for determining the relative binding affinity of a test molecule
CC to CCR5 and a computer aided drug screening assay that utilises the
CC three-dimensional structure of CCR5. Compounds identified using the
CC methods of the invention are useful for treating or preventing HIV
CC (human immunodeficiency virus) infection or AIDS (acquired
CC immunodeficiency syndrome) in a patient. The methods of the invention
CC may also be used to identify agonists or antagonists of the interaction
CC of CCR5 with its natural ligand, and to determine a binding motif for
CC CCR5. The present sequence represents human CCR5.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 1841; DB 23; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-200;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy 181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
Db 181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy 241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352

RESULT 11
AAY41280
ID AAY41280 standard; Protein; 439 AA.
XX
AC AAY41280;
XX
DT 11-FEB-2000 (first entry)
XX
DE Fusion protein containing human chemokine receptor CCR-5.
XX
KW Prostaglandin; PG; E2EP3 receptor; E2EP2 receptor; CCR-5; human;
KW chemokine receptor; ss2 adrenergic receptor; small G-protein rho;
KW renal outer medullary potassium ion channel protein; ion-channel protein;
KW lambda phage repressor protein; G-protein coupled receptor; bacteria;
KW biochemical; vaccine; immunohistochemical; orphan receptor; HIV.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953033-A1.
XX
PD 21-OCT-1999.
XX
PF 16-APR-1999; 99WO-US08214.
XX
PR 16-APR-1998; 98US-0081989.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Breyer RM, Ma L, Kennedy C;
XX
DR WPI; 1999-620416/53.
DR N-PSDB; AAZ24738.
XX
PT New nucleic acid constructs for high level expression of eukaryotic
PT proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for
PT preventing HIV infection
XX
PS Disclosure; Page 49-53; 81pp; English.
XX
CC The invention provides isolated nucleic acid sequences that encode rabbit
CC prostaglandin (PG) E2EP3 receptor, human PG E2EP2 receptor, human
CC chemokine receptor CCR-5, human ss2 adrenergic receptor, rat renal outer
CC medullary potassium ion channel protein or human small G-protein rho,
CC together with deduced protein sequences. Also provided is a method for
CC the production of eukaryotic proteins by culturing bacteria transformed
CC with vectors containing the above nucleic acid sequences or a nucleic
CC acid (I) that comprises: (i) first sequence that encodes either a
CC sequence comprising at least three positively charged amino acids, or a
CC DNA-binding protein, or a lambda phage repressor protein, placed upstream
CC of, and in frame with, (ii) a sequence encoding a protein. (I) are used
CC for recombinant production of eukaryotic proteins, particularly membrane
CC proteins, G-protein coupled receptors or ion-channel proteins, in
CC bacteria. These proteins are useful for biochemical or structural
CC studies; as therapeutic agents; in diagnostic and screening assays and as
CC antigens for use in vaccines, and for raising antibodies that are useful
CC as immunohistochemical markers, e.g. for orphan receptors or ion
CC channels. Antibodies raised against the chemokine receptor CCR-5 can be
CC used (when administered as antiserum or generated in vivo) to prevent
CC entry of human immune deficiency virus (HIV) into cells.
XX
SQ Sequence 439 AA;

Query Match 100.0%; Score 1841; DB 20; Length 439;
Best Local Similarity 100.0%; Pred. No. 4.8e-200;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
Db 79 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 138

Qy 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
Db 139 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 198

Qy 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
Db 199 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 258

Qy 181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
Db 259 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 318

Qy 241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
Db 319 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 378

Qy 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
Db 379 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 430

RESULT 12
AAW23834
ID AAW23834 standard; Protein; 371 AA.
XX
AC AAW23834;
XX
DT 08-JUN-1998 (first entry)
XX
DE Human CC chemokine receptor 5 (CCR5) A127V variant.
XX
KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW transgenic animal.

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          48..74
FT                   /label= I
FT                   /note= "transmembrane domain"
FT   Domain          123..145
FT                   /label= III
FT                   /note= "transmembrane domain"
FT   Domain          162..190
FT                   /label= IV
FT                   /note= "transmembrane domain"
FT   Domain          213..238
FT                   /label= V
FT                   /note= "transmembrane domain"
FT   Domain          257..277
FT                   /label= VI
FT                   /note= "transmembrane domain"
FT   Domain          296..319
FT                   /label= VII
FT                   /note= "transmembrane domain"
XX
PN   WO9745543-A2.
XX
PD   04-DEC-1997.
XX
PF   28-MAY-1997;   97WO-US09586.
XX
PR   28-MAY-1996;   96US-0018508.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Alkhatib G,  Berger EA,  Broder CC,  Combadiere C;
PI   Feng Y,  Kennedy PE, Murphy PM;
XX
DR   WPI; 1998-032650/03.
DR   N-PSDB; AAT76919.
XX
PT   CC chemokine receptor 5 polypeptide - used to inhibit membrane
PT   fusion between HIV and a target cell
XX
PS   Example 1; Fig 1B; 70pp; English.
XX
CC   This protein sequence comprises an Ala127Leu variant of a novel
CC   human macrophage-selective CC chemokine receptor (see also
CC   AAW23835) that has been designated CCR5.  The sequence was deduced
CC   from an isolated cDNA clone (see AAT76919).  The conservative
CC   variation should not affect the activity of CCR5.  The susceptibility
CC   of human macrophages to HIV infection depends on cell surface
CC   expression of CD4 and CCR5.  CCR5 is a member of the 7-transmembrane
CC   superfamily of G-protein coupled cell surface molecules.  It plays
CC   an essential role in the membrane fusion step of infection by some
CC   HIV isolates.  The establishment of stable, non-human cell lines
CC   and transgenic mammals having cells that coexpress human CD4 and
CC   CCR5 provides valuable tools for research of HIV infection.
CC   Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
CC   agents capable of blocking membrane fusion between HIV and target
CC   cells represent potential anti-HIV therapeutics for macrophage
CC   tropic strains of HIV.
XX
SQ   Sequence   371 AA;

  Query Match             99.7%;  Score 1836;  DB 19;  Length 371;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-199;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 79

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||

Db         80 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 139

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 199

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 259

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 319

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 371


RESULT 13
ABB56342
ID   ABB56342 standard; Protein; 352 AA.
XX
AC   ABB56342;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Non-endogenous human GPCR protein, SEQ ID NO: 477.
XX
KW   Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW   constitutively activated GPCR; agonist; disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177172-A2.
XX
PD   18-OCT-2001.
XX
PF   05-APR-2001; 2001WO-US11098.
XX
PR   07-APR-2000; 2000US-195747P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Lehmann-Bruinsma K,  Liaw CW,  Lin I;
XX
DR   WPI; 2001-648759/74.
DR   N-PSDB; ABI97978.
XX
PT   Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT   disease treatment, comprises contacting candidate compounds with
PT   versions of GPCRs -
XX
PS   Claim 1; Page 277-278; 394pp; English.
XX
CC   The invention relates to G protein-coupled receptors (GPCRs) for which
CC   the endogenous ligand has been identified. Non-endogenous
CC   constitutively activated versions of known GPCRs are used in the
CC   invention for the direct identification of candidate compounds as
CC   receptor agonists, inverse agonists or partial agonists. Such
CC   agonists are useful as therapeutic agents for diseases or disorders
CC   associated with GPCRs. The present sequence is a non-endogenous
CC   version of a known human GPCR.
XX
SQ   Sequence   352 AA;

  Query Match             99.7%;  Score 1835;  DB 22;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 1.7e-199;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAKRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 14
AAM52829
ID   AAM52829 standard; Protein; 352 AA.
XX
AC   AAM52829;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Human CCR5 Gln 55 variant.
XX
KW   CCR5; CC chemokine receptor 5; human; HIV infection;
KW   human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW   drug screening; identification; variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "Glu replaces wild-type Leu; encoded by CTG"
FT   Misc-difference 58
FT                   /note= "Encoded by AGC"
XX
PN   WO200171346-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US09155.
XX
PR   21-MAR-2000; 2000US-190946P.
PR   21-MAR-2000; 2000US-190996P.
PR   21-MAR-2000; 2000US-191299P.
PR   20-MAR-2001; 2001US-0813448.
PR   20-MAR-2001; 2001US-0813651.
PR   20-MAR-2001; 2001US-0813653.
XX
PA   (CONS-) CONSENSUS PHARM INC.
XX
PI   Nestor JJ,  Wilson CJ,  See RH,  Tan Hehir CA;
XX
DR   WPI; 2002-010610/01.
DR   N-PSDB; ABA02318.
XX
PT   Identifying CC chemokine receptor 5 binding compound for treating AIDS,
PT   comprises binding a molecule from library to a molecule having binding
PT   property corresponding to CCR5 and identifying bound molecule  -
XX
PS   Example 3; Fig 4B; 50pp; English.
XX
CC   The invention relates to a method for*identifying a binding compound
CC   for CC chemokine receptor 5 (CCR5). The method involves screening a
CC   library of test molecules (particularly peptides) with immobilised CCR5,
CC   and then identifying those molecules which bind. The invention also
CC   relates to CCR5-binding molecules identified using the method of the
CC   invention, methods for identifying consensus motifs for CCR5-binding
CC   peptides, a transfer vector encoding tagged CCR5, a computer-aided
CC   methods for determining the relative binding affinity of a test molecule
CC   to CCR5 and a computer aided drug screening assay that utilises the
CC   three-dimensional structure of CCR5. Compounds identified using the
CC   methods of the invention are useful for treating or preventing HIV
CC   (human immunodeficiency virus) infection or AIDS (acquired
CC   immunodeficiency syndrome) in a patient. The methods of the invention
CC   may also be used to identify agonists or antagonists of the interaction
CC   of CCR5 with its natural ligand, and to determine a binding motif for
CC   CCR5. The present sequence represents a naturally occurring variant of
CC   human CCR5 in which there is a glutamine, rather than a leucine, at
CC   position 55.
XX
SQ   Sequence   352 AA;

  Query Match             99.7%;  Score 1835;  DB 23;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 1.7e-199;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILIQINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 15
AAE07039
ID   AAE07039 standard; Protein; 352 AA.
XX
AC   AAE07039;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX
KW   Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW   human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
KW   cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
KW   neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW   rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW   gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW   haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW   multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW   cardiovascular disorder; myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO200158915-A2.
XX
PD   16-AUG-2001.
```

XX
PF 09-FEB-2001; 2001WO-US04152.
XX
PR 09-FEB-2000; 2000US-0181258.
PR 09-MAR-2000; 2000US-0187999.
PR 22-SEP-2000; 2000US-0234336.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI; 2001-488965/53.
DR N-PSDB; AAD13198.
XX
PT Isolated nucleic acid encoding a human G-protein chemokine receptor
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating
PT autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
PT disorders and neurodegenerative disorders -
XX
PS Example 40; Page 486-487; 495pp; English.
XX
CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing
CC or ameliorating a disease or disorder associated with inflammation,
CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
CC aberrant T-cell antigen presenting cell interaction. The disease or
CC disorder may also be an infectious disease (e.g. a viral infection such
CC as an early stage HIV infection, a cytomegalovirus infection, or a
CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
CC a neurodegenerative disorder. The disease or disorder may be associated
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
CC is used as a food additive or preservative to increase or decrease
CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
CC antibodies, agonists and antagonists are also useful in the
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis); cardiovascular disorders (myocardial ischaemias) and
CC wound healing.
XX
SQ Sequence 352 AA;

Query Match 99.6%; Score 1833; DB 22; Length 352;
Best Local Similarity 99.7%; Pred. No. 2.9e-199;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTEEQEISVGL 352
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Search completed: June 3, 2003, 15:19:02
Job time : 66.5644 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:16:36 ; Search time 32.2822 Seconds
(without alignments)
1048.235 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	100.0	352	2	A43113	chemokine (C-C) re
2	1364	74.1	360	2	JC2443	chemokine (C-C) re
3	1224	66.5	374	2	I38450	chemokine (C-C) re
4	1055	57.3	355	2	A45177	chemokine (C-C) re
5	1007.5	54.7	355	2	I49339	macrophage inflamm
6	1001.5	54.4	359	2	I49341	MIP-1 alpha recept
7	935.5	50.8	355	2	G02436	chemokine (C-C) re
8	919	49.9	360	2	A57160	chemokine (C-C) re
9	906	49.2	360	2	JC4587	chemokine (C-C) re
10	829	45.0	383	2	S55594	G protein-coupled
11	799.5	43.4	356	2	I49340	MIP-1 alpha recept
12	746.5	40.5	355	2	JC5067	G protein-coupled
13	712	38.7	354	2	I58186	probable G protein
14	673	36.6	344	2	JC5942	chemokine receptor
15	670.5	36.4	355	2	JC4304	orphan G protein-c
16	567	30.8	378	2	B55735	lymphocyte-specifi
17	562	30.5	378	2	A55735	G protein-coupled
18	559	30.4	369	2	JC5068	G protein-coupled
19	553	30.0	378	2	A45680	G protein-coupled
20	541	29.4	333	2	I65989	G protein-coupled
21	521	28.3	360	2	A53611	interleukin-8 rece
22	517.5	28.1	359	2	A48921	interleukin-8 rece
23	515	28.0	355	2	JQ1231	interleukin-8 rece
24	514.5	27.9	358	2	A53752	interleukin-8 rece
25	510.5	27.7	367	2	JE0349	interferon-inducib
26	509.5	27.7	350	2	JN0621	G protein-coupled
27	506.5	27.5	350	2	A39445	interleukin-8 rece
28	506	27.5	352	2	G00048	fusin (LESTRA) - c
29	506	27.5	352	2	A45747	neuropeptide Y/pep
30	496.5	27.0	353	2	S28787	neuropeptide Y/pep
31	490.5	26.6	356	2	S42096	interleukin-8 rece
32	474.5	25.8	359	2	JC2134	angiotensin II rec
33	473.5	25.7	359	2	A42656	angiotensin II rec
34	472	25.6	374	2	S42628	G protein-coupled
35	471	25.6	359	2	I51372	angiotensin II rec
36	469.5	25.5	359	2	JH0621	angiotensin II rec
37	468.5	25.4	359	2	S44425	angiotensin II rec
38	468.5	25.4	359	2	JC1194	angiotensin II rec
39	466.5	25.3	359	2	S15403	angiotensin II rec
40	464.5	25.2	359	2	JQ1516	angiotensin II rec
41	461.5	25.1	359	2	JC1104	angiotensin II rec
42	461	25.0	327	2	S56162	MDCR15 protein - h
43	461	25.0	372	2	S26667	G protein-coupled
44	460.5	25.0	359	2	A48857	angiotensin II rec
45	453	24.6	374	2	S32785	G protein-coupled

ALIGNMENTS

RESULT 1
A43113
chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine rece
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarag
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184,'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a d
nd may have had a selective advantage by conferring resistance to Yersinia plague inf
R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine
A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemok
A;Reference number: A58833; MUID:96291862; PMID:8663314

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A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTE
A;Note: probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F;32-56/Domain: transmembrane #status predicted <TM1>
F;67-87/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;142-166/Domain: transmembrane #status predicted <TM4>
F;193-218/Domain: transmembrane #status predicted <TM5>
F;236-257/Domain: transmembrane #status predicted <TM6>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

  Query Match           100.0%;  Score 1841;  DB 2;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-145;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmemb
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

  Query Match           74.1%;  Score 1364;  DB 2;  Length 360;
  Best Local Similarity  75.5%;  Pred. No. 2.1e-105;
  Matches  259;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    2;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||:||||||:||||||: |||   | |  :||    :
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   ||||||||||:||||||||||||||||||||||:|||||||||||
Db        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
              |||||:|||||||||||:|| |:::|||| ||||||||||||||||||||| ||
Db        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317

Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||:||| ||||| | :| :|  :  :|  | ||||||:| ||
Db        318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360


RESULT 3
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte c
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38450
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
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C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F;44-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM6>
F;292-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;32-277,113-190/Disulfide bonds: #status predicted

  Query Match             66.5%;  Score 1224;  DB 2;  Length 374;
  Best Local Similarity   76.3%;  Pred. No. 8.2e-94;
  Matches  235;  Conservative   27;  Mismatches   34;  Indels   12;  Gaps    3;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||||||||||||||:||||||:||||||: |||   | |  :||    :
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197

Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              | || |:   |||||||||:|||||||||||||||||||||||:||||||||||
Db        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
              |||||:|||||||||||:|| |:::|||| |||||||||||||||||||||||:
Db        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316

Qy        310 VFFQKHIA 317
                 |||
Db        317 -----HIA 319


RESULT 4
A45177
chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-
A;Reference number: A45177; MUID:93161416; PMID:7679328
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alph
A;Reference number: I55671; MUID:93240122; PMID:7683036
A;Accession: I55671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte

  Query Match             57.3%;  Score 1055;  DB 2;  Length 355;
  Best Local Similarity   56.1%;  Pred. No. 7.4e-80;
  Matches  197;  Conservative   59;  Mismatches   89;  Indels    6;  Gaps    4;

Qy          2 DYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL 61
              ||  ::   : :|  : ||||:| :   |:||||||||||: | |||:||:|:|:  |||
Db          9 DYDTTT---EFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYKRL 65

Qy         62 KSMTDIYLLNLAISDLFFLLTVPFWAHYAAA-QWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |:|| |||||||||| || |:||  |     | ||: ||::|:| |: | :| |||||
Db         66 KNMTSIYLLNLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFFII 125

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||:||||||:||:| | :|: ||:||: |:::| |  |:|||
Db        126 LLTIDRYLAIVHAVFALRARTVTFGVITSIIIWALAILASMPGLYFSKTQWEFTHHTCSL 185

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              |||:   : || || ||: : |||||||||:|||:||:| |||  ||||  :||||| |
Db        186 HFPHESLREWKLFQALKLNLFGLVLPLLVMIICYTGIIKILLRRPNEKK-SKAVRLIFVI 244

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||::|||| |||: :|:: ||:|   : |  |  || |:|||| :  ||||:||:|||||
Db        245 MIIFFLFWTPYNLTILISVFQDFLFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYAFV 304

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVG 351
              ||:|| ||   | : :|    |       :  || ||  : |||| |:| |
Db        305 GERFRKYLRQLFHRRVAVHLVKWLPFLSVDRLERVSST-SPSTGEHELSAG 354


RESULT 5
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chem
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <RES>
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin

  Query Match             54.7%;  Score 1007.5;  DB 2;  Length 355;
  Best Local Similarity   55.6%;  Pred. No. 6.2e-76;
  Matches  190;  Conservative   55;  Mismatches   94;  Indels    3;  Gaps    3;

Qy         11 DINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLL 70
              : :|  | ||||  |:   | |||||||||||| | |||:||||:|:  :||:||| |||
Db         15 EFDYGDSTPCQKTAVRAFGAGLLPPLYSLVFIIGVVGNVLVILVLMQHRRLQSMTSIYLF 74

Qy         71 NLAISDLFFLLTVPFWAHYAAA-QWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||:||| || |:|||  |     | ||: ||:||:| |::| :| ||||||||||||||
Db         75 NLAVSDLVFLFTLPFWIDYKLKDDWIFGDAMCKLLSGFYYLGLYSEIFFIILLTIDRYLA 134

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
              :|||||||:||||| |::||:||| :|: ||:| : | ::| |  | ||| ||||   :
Db        135 IVHAVFALRARTVTLGIITSIITWALAILASMPALYFFKAQWEFTHRTCSPHFPYKSLKQ 194
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Qy        190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
              || || ||: :|||:||||||:|||:||:: ||| |  :|: :|||||| | :::|| |
Db        195 WKRFQALKLNLLGLILPLLVMIICYAGIIRILLR-RPSEKKVKAVRLIFAITLLFFLLWT 253

Qy        250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
              |||: : :: ||:    | |  |  || |||||| :  ||||:||||| ||||:|  ||
Db        254 PYNLSVFVSAFQDVLFTNQCEQSKHLDLAMQVTEVIAYTHCCVNPIIYVFVGERFWKYLR 313

Qy        310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVG 351
                ||:|:|    |       :  || ||: : |||| |:| |
Db        314 QLFQRHVAIPLAKWLPFLSVDQLERTSSI-SPSTGEHELSAG 354


RESULT 6
I49341
MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C;Accession: I49341
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

  Query Match             54.4%;  Score 1001.5;  DB 2;  Length 359;
  Best Local Similarity   56.2%;  Pred. No. 2e-75;
  Matches  190;  Conservative   55;  Mismatches   90;  Indels    3;  Gaps    3;

Qy         14 YYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLA 73
              |  : ||:|: :|:: : |||||||||||| | :|||:|:|||||  ::|: ||:||| |||
Db         22 YEWAPPCEKVRIKELGSWLLPPLYSLVFIIGLLGNMMVVLILIKYRKLQIMTNIYLFNLA 81

Qy         74 ISDLFFLLTVPFWAHYAA-AQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVH 132
              |||| || ||||| ||    :| ||: ||::|:| |::  :| |||||||||||||:||
Db         82 ISDLLFLFTVPFWIHYVLWNEWGFGHYMCKMLSGFYYLALYSEIFFIILLTIDRYLAIVH 141

Qy        133 AVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKN 192
              |||||:||||||  :||:||| :|  |:||  ||  ||     ::||  :|  :   ||
Db        142 AVFALRARTVTFATITSIITWGLAGLAALPEFIFHESQDSFGEFSCSPRYPEGEEDSWKR 201

Qy        193 FQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYN 252
              |  |:: | || ||||||||||||||:|||||| | ||:|:|:|:|||| :|||:|:|| |||
Db        202 FHALRMNIFGLALPLLVMVICYSGIIKTLLRCPN-KKKHKAIRLIFVVMIVFFIFWTPYN 260

Qy        253 IVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFF 312
              :||| : |   |   :|  |  || |||||| :  ||||:||:|||||||:|| :| :||
Db        261 LVLLFSAFHSTFLETSCEQSKHLDLAMQVTEVIAYTHCCVNPVIYAFVGERFRKHLRLFF 320

Qy        313 QKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISV 350
              :::   :       |   | ||| : |||||||||
Db        321 HRNVQFTWENIFQFLPGEENGRTSSV-SPSTGEQEISV 357


RESULT 7
G02436
chemokine (C-C) receptor 3 - human
N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accession: G02436; A57237
R;Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A;Reference number: H01272
A;Accession: G02436
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <PON>
A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561
R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine recepto
A;Reference number: A57237; MUID:95348056; PMID:7622448
A;Accession: A57237
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504
C;Genetics:
A;Gene: GDB:CMKBR3
A;Cross-references: GDB:579624; OMIM:601268
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte

  Query Match             50.8%;  Score 935.5;  DB 2;  Length 355;
  Best Local Similarity   53.0%;  Pred. No. 5.6e-70;
  Matches  176;  Conservative   63;  Mismatches   90;  Indels    3;  Gaps    3;

Qy         20 CQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFF 79
              |:| : : : |: :||||||||  | :||::|::|||  :||: ||:|||||||||| |
Db         24 CEKADTRALMAQFVPPLYSLVFTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLF 83

Qy         80 LLTVPFWAHYAAA-QWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALK 138
              |:|:||| ||     | ||: ||:||:| |  | :| ||||||||||||:|||||:
Db         84 LVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Qy        139 ARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTLKI 198
              ||||||||:||::|| :|| |:||  ||  :::      ||: :|      |::| ||::
Db        144 ARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTVYSWRHFHTLRM 203

Qy        199 VILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLN 258
              .|  |||||||| |||:||:|||||| : ||:::|:|||| || |:|:|| |||: :||:
Db        204 TIFCLVLPLLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIFWTPYNVAILLS 262

Qy        259 TFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAK 318
              ::|     |:|  :  ||  | ||| :  :|||:||:|||||||:|| ||  || :|:
Db        263 SYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRHLLM 322

Qy        319 RFCKCCSIFQQEAPERASSVYTRSTGEQEISV 350
                :       |  || ||| : || | |:|:
Db        323 HLGRYIPFLPSEKLERTSSV-SPSTAEPELSI 353


RESULT 8
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
```

```
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match             49.9%;  Score 919;  DB 2;  Length 360;
  Best Local Similarity   49.9%;  Pred. No. 1.3e-68;
  Matches  176;  Conservative   68;  Mismatches   99;  Indels   10;  Gaps    6;

Qy          2 DYQVSSPIYDINYYTSE----PCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILIN 57
              |  :   ||  |||  |    || |  :|      |||||||||:|| :|| :|:|:|
Db          8 DTTLDESIYS-NYYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFK 66

Qy         58 CKRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIF 117
               |||:||||:|||||||||| |: ::||| :||| || ||  :|:::: :| :||:||||
Db         67 YKRLRSMTDVYLLNLAISDLLFVFSLPFWGYYAADQWVFGLGLCKMISWMYLVGFYSGIF 126

Qy        118 FIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYT 177
              |::|::|||||:|||||:|:|||:|:||:||: || |||||||| :|:    |  |
Db        127 FVMLMSIDRYLAIVHAVFSLRARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTY 186

Qy        178 CSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLI 237
              | : :  :    ||   :|:| |||||:|| :|: ||| |::||  |:|||| ::||::|
Db        187 CKTKYSLNS-TTWKVLSSLEINILGLVIPLGIMLFCYSMIIRTLQHCKNEKK-NKAVKMI 244

Qy        238 FTIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIY 297
              | :::::  || |||||| | |  |    | :|:    || |:| |||   |||:|||||
Db        245 FAVVVLFLGFWTPYNIVLFLETLVELEVLQDCTFERYLDYAIQATETLAFVHCCLNPIIY 304

Qy        298 AFVGEKFRNYLLVFFQKHIAKRF--CKCCSIFQQEAPERASSVYTRSTGEQEI 348
               |:|||| |:|  | |     |  |: | : |  : :  || ||:|| : ::
Db        305 FFLGEKFRKYILQLF-KTCRGLFVLCQYCGLLQIYSADTPSSSYTQSTMDHDL 356


RESULT 9
JC4587
chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match             49.2%;  Score 906;  DB 2;  Length 360;
  Best Local Similarity   49.9%;  Pred. No. 1.6e-67;
  Matches  171;  Conservative   69;  Mismatches   97;  Indels    6;  Gaps    4;

Qy          9 IYDINYY---TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMT 65
              :|:  |:      :|| |  :|      |||||||||: |  || :|:|:|   |||||||
Db         15 VYNSYYFYESMPKPCTKEGIKAFGEVFLPPLYSLVFLLGLFGNSVVVLVLFKYKRLKSMT 74

Qy         66 DIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTID 125
              |:|||||||||| |:|::||| :||| || ||  :|:::: :| :|||:||||||:|::||
Db         75 DVYLLNLAISDLLFVLSLPFWGYYAADQWVFGLGLCKIVSWMYLVGFYSGIFFIMLMSID 134

Qy        126 RYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYS 185
              ||||:|||||:|||||:|:||:||:||:||| ||||||||::|:    |  |  | : :  :
Db        135 RYLAIVHAVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTCYTEHNHTYCKTQYSVN 194

Qy        186 QYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYF 245
                  ||   :|:| :|||::|| :|:  || |::||  |:|||| :||||:|| :::::
Db        195 S-TTWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLQHCKNEKK-NRAVRMIFGVVVLFL 252

Qy        246 LFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFR 305
              || |||:|| | |  |   | :|:    || |:| |||||  |||:|||:|| |:|||||
Db        253 GFWTPYNVVLFLETLVELEVLQDCTLERYLDYAIQATETLGFIHCCLNPVIYFFLGEKFR 312

Qy        306 NYLLVFFQKHIAKR-FCKCCSIFQQEAPERASSVYTRSTGEQE 347
              |:   |:          || |   |  : : :|| ||:|| : :
Db        313 KYITQLFRTCRGPLVLCKHCDFLQVYSADMSSSSYTQSTVDHD 355


RESULT 10
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S55594
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-383 <TEL>
A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match             45.0%;  Score 829;  DB 2;  Length 383;
  Best Local Similarity   47.4%;  Pred. No. 3.9e-61;
  Matches  157;  Conservative   64;  Mismatches  102;  Indels    8;  Gaps    3;

Qy         11 DINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLL 70
              |::|  | || | :  ::||:::| || |||:|| :||:||::|:|   ::|::|:: ||
Db         53 DVDYEESAPCYKSDTTRLAAQVVPALYLLVFLFGLLGNILVVIIVIRYMKIKNLTNMLLL 112

Qy         71 NLAISDLFFLLTVPFWAHYAAA--QWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYL 128
              ||||||| ||||:||| ||       | || ::|:|| |: ::  :| :| |||||:||||
Db        113 NLAISDLLFLLTLPFWMHYIGMYHDWTFGISLCKLLRGVCYMSLYSQVFCIILLTVDRYL 172

Qy        129 AVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQ 188
              |||:|| ||: |||| |:|| | || :|   |||   |   | :     |  ::|
Db        173 AVVYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFHGHQDDNGRVQCDPYYPEMSTN 232

Qy        189 FWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFW 248
              |:     |:::| |:||||:| :||  |:: ||| |  ||:::|:|||| ||: ||:||
Db        233 VWRRAHVAKVIMLSLILPLLIMAVCYYVIIRRLLR-RPSKKKYKAIRLIFVIMVAYFVFW 291

Qy        249 APYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYL 308
              |||||||:|:||       |: |: || |: :|:|:  |||||||:||||||||| :|
Db        292 TPYNIVLLLSTFHATLLNLQCALSSNLDMALLITKTVAYTHCCINPVIYAFVGEKFRRHL 351

Qy        309 LVFFQKHIAKRFCKCCSIFQ-----QEAPER 334
              ||  ::|   ||           :| | |
Db        352 YHFFHTYVAIYLCKYIPFLSGDGEGKEGPTR 382
```

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RESULT 11
I49340
MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-356 <RES>
A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin

  Query Match             43.4%;  Score 799.5;  DB 2;  Length 356;
  Best Local Similarity   45.0%;  Pred. No. 9.9e-59;
  Matches  159;  Conservative   68;  Mismatches  119;  Indels    7;  Gaps    4;

Qy          5 VSSPIYDI----NYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |: | |:     :: :   |  |||:     :  |||||||| | :|::||:|:||  ||
Db          6 VTEPSYNTVAKNDFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVVLVLIQHKR 65

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHY-AAAQWDFGNTMCQLLTGLYFIGFFSGIFFI 119
              |::|| ||| ||||||| || |:|||   |      | ||| ||: ::| |::| :| :|||
Db         66 LRNMTSIYLFNLAISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYYLGLYSDMFFI 125

Qy        120 ILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCS 179
               |||||||||||| ||||:|||||||:::|:|||||:|   |:| :   :|| |  ::||
Db        126 TLLTIDRYLAVVHVVFALRARTVTFGIISSIITWVLAALVSIPCLYVFKSQMEFTYHTCR 185

Qy        180 SHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFT 239
              :  |      :  || | : ||||:|||| |:|||: |:  | | |  ||: : :||||
Db        186 AILPRKSLIRFLRFQALTMNILGLILPLLAMIICYTRIINVLHR-RPNKKKAKVMRLIFV 244

Qy        240 IMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAF 299
              | :::||  ||| :   :: |::     :|  | ::| :: :|| |  ||||:||:|| |
Db        245 ITLLFFLLLAPYYLAAFVSAFEDVLFTPSCLRSQQVDLSLMITEALAYTHCCVNPVIYVF 304

Qy        300 VGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||::|| ||   |::| |    :      ::  :|||:    || | | |  |
Db        305 VGKRFRKYLWQLFRRHTAITLPQWLPFLSEDRAQRASA-RLPSTVEIETSADL 356


RESULT 12
JC5067
G protein-coupled receptor CKR-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Accession: JC5067; G02776; G02387
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5067
A;Molecule type: DNA
A;Residues: 1-355 <ZAB>
A;Cross-references: EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01714
A;Accession: G02776
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R;Bonner, T.I.
submitted to the EMBL Data Library, January 1996
A;Reference number: H01154
A;Accession: G02387
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <BON>
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
A;Cross-references: GDB:6053733; OMIM:601834
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;36-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;200-222/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM6>
F;281-304/Domain: transmembrane #status predicted <TM7>

  Query Match             40.5%;  Score 746.5;  DB 2;  Length 355;
  Best Local Similarity   41.1%;  Pred. No. 2.4e-54;
  Matches  148;  Conservative   66;  Mismatches  125;  Indels   21;  Gaps    6;

Qy          1 MDYQVSSPIYDI-NYY----TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILIL 55
              ||| :   :  : :||     | ||    ::     ||   | |:|:|  :|| ||||:|
Db          1 MDYTLDLSVTTVTDYYYPDIFSSPCDAELIQTNGKLLLAVFYCLLFVFSLLGNSLVILVL 60

Qy         56 INCKRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSG 115
              : ||:|:|:||:||||||:||| |: : ||  :|   || ||  ||::::| |:|||:|
Db         61 VVCKKLRSITDVYLLNLALSDLLFVFSFPFQTYYLLDQWVFGTVMCKVVSGFYYIGFYSS 120

Qy        116 IFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLH 175
              :||| |:::|||||||||||:||| ||:  |    :  |: |: |::| ::| :   |
Db        121 MFFITLMSVDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGV 180

Qy        176 YTCSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVR 235
              | | |   |  || |  |: ||||::|  : : ||  ||  | ||:|  |  :|:|
Db        181 LQCYS-FYNQQTLKWKIFTNFKMNILGLLIPFTIFMFCYIKILHQLKRCQNHNKT-KAIR 238

Qy        236 LIFTIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPI 295
              |:  ::|   ||| |:|:|| | :      |: || | :|  |  ||| :  ||||:||:
Db        239 LVLIVVIASLLFWVPFNVVLFLTSLHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPV 298

Qy        296 IYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQ-------QEAPERASSVYTRSTGEQEI 348
              |||||||||: :|   |||        |  ||        :|: |::||    |:    :
Db        299 IYAFVGEKFKKHLSEIFQK-------SCSQIFNYLGRQMPRESCEKSSSCQQHSSRSSSV 351


RESULT 13
I58186
probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: I58186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord an
A;Reference number: I58186; MUID:94323113; PMID:8047298
A;Accession: I58186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match             38.7%;  Score 712;  DB 2;  Length 354;
  Best Local Similarity   40.6%;  Pred. No. 1.7e-51;
  Matches  147;  Conservative   59;  Mismatches  126;  Indels   30;  Gaps    6;

Qy          6 SSPIYDINYY----TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL 61
```

```
                 | |  |:  :    ::| |   ::       |   ||||| || |||:||:| | | ::
Db          4 SFPELDLENFEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTFGLVGNLLVVLALTNSRKS 63

Qy         62 KSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIIL 121
               ||:|||||||||:||| |: |:||| ||  :     | ||:| |  :||||| ||||| :
Db         64 KSITDIYLLNLALSDLLFVATLPFWTHYLISHEGLHNAMCKLTTAFFFIGFFGGIFFITV 123

Qy        122 LTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSH 181
               ::||||||:| |  ::  |||  ||  |:  |  |:  : |  :||: :       |
Db        124 ISIDRYLAIVLAANSMNNRTVQHGVTISLGVWAAAILVASPQFMFTKRKDN----ECLGD 179

Qy        182 FPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIM 241
               :|    : |   :  :: ||| |||||:|  ||  |::||  |:| ||  ||:|||  ::
Db        180 YPEVLQEIWPVLRNSEVNILGFVLPLLIMSFCYFRIVRTLFSCKNRKKA-RAIRLILLVV 238

Qy        242 IVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVG 301
               :|:|||| |||||: | | : :    :|     |  |: ||||:  :|||:|| |||| |
Db        239 VVFFLFWTPYNIVIFLETLKFYNFFPSCGMKRDLRWALSVTETVAFSHCCLNPFIYAFAG 298

Qy        302 EKFRNYLLVFFQKHIAKRFCKCCSIF----------QQEAPERASSVYTRSTGEQEI 348
               |||| ||     :|:   : || ::              |:   :   |  |  | | |
Db        299 EKFRRYL-----RHL---YNKCLAVLCGRPVHAGFSTESQRSRQDSILSSLTHYTSEGEG 350

Qy        349 SV 350
               |:
Db        351 SL 352


RESULT 14
JC5942
chemokine receptor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5942
R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor.
A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <FAN>
A;Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
C;Superfamily: vertebrate rhodopsin

  Query Match             36.6%;  Score 673;  DB 2;  Length 344;
  Best Local Similarity   40.9%;  Pred. No. 2.8e-48;
  Matches  137;  Conservative   64;  Mismatches  108;  Indels   26;  Gaps    7;

Qy         17 SEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISD 76
               :| |  : : ::|:|:| | | ||: | : |:|||:|||:  | || : :|||||||:|:
Db         25 AEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAVSN 84

Qy         77 LFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVH-AVF 135
               | ||||:|||||         |: ||::| ||||:| :|  ||  |||: |||  :|   |
Db         85 LCFLLTLPFWAHAG------GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKGNF 138

Qy        136 ALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCS-SHFPY--SQYQFWKN 192
               | |  |::|||: || |: |:||  :  : | |   | |: |  |:  :   |||:
Db        139 FSARRRVPCGIITSVLAWVTAILATLPEYVVYKPQMEDQKYKCAFSRTPFLPADETFWKH 198

Qy        193 FQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYN 252
               | |||: |  ||||| :    |  : |||   |  ::|:   :|:| ||:|: | |||||
Db        199 FLTLKMNISVLVLPLFIFTFLYVQMRKTL---RFREQRYSLFKLVFAIMVVFLLMWAPYN 255

Qy        253 IVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFF 312
               |   |:||:| | |::| ||  ||::: :|: :  |||||||::|||:   |  ||
Db        256 IAFFLSTFKEHFSLSDCKSSYNLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYL---- 311

Qy        313 QKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQE 347
                     |:| : :   | :     : |  :|
Db        312 --------CRCFHL-RSNTPLQPRGQSAQGTSREE 337


RESULT 15
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related t
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular sig
C;Comment: This protein is a key regulator of many immune and homeostatic responses,
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

  Query Match             36.4%;  Score 670.5;  DB 2;  Length 355;
  Best Local Similarity   42.9%;  Pred. No. 4.6e-48;
  Matches  129;  Conservative   55;  Mismatches  112;  Indels    5;  Gaps    3;

Qy         17 SEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISD 76
               :| |   ::       |   ||::|  | |||:||:  | | |: ||:|||||||||:||
Db         18 AEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSD 77

Qy         77 LFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFA 136
               | |: |:||| ||    :    | ||:  |  :|||||  |||| :::|||||||:| |  :
Db         78 LLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANS 137

Qy        137 LKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTL 196
               :  |||  ||  |:  |  |:  : |  :||: |||     |   :|    : |   : :
Db        138 MNNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKEN---ECLGDYPEVLQEIWPVLRNV 193

Qy        197 KIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLL 256
               :   || :||||:|  ||  |::||  |:| ||  :|::||  ::|||:|||| |||:::
Db        194 ETNFLGFLLPLLIMSYCYFRIIQTLFSCKNHKKA-KAIKLILLVVIVFFLFWTPYNVMIF 252

Qy        257 LNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHI 316
               | | : :    :|      |  |: ||||:  :|||:||:|||| ||||| ||   : | :
Db        253 LETLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYLYHLYGKCL 312

Qy        317 A 317
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Db        313 A 313


Search completed: June  3, 2003, 15:22:40
Job time : 34.2822 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:09:40 ; Search time 16.1411 Seconds
(without alignments)
904.503 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	100.0	352	1	CKR5_HUMAN	P51681 homo sapien
2	1835	99.7	352	1	CKR5_PANTR	P56440 pan troglod
3	1830	99.4	352	1	CKR5_PONPY	O97881 pongo pygma
4	1825	99.1	352	1	CKR5_GORGO	P56439 gorilla gor
5	1821	98.9	352	1	CKR5_TRAPH	O97879 trachypithe
6	1816	98.6	352	1	CKR5_PAPHA	P56441 papio hamad
7	1816	98.6	352	1	CKR5_TRAFR	O97878 trachypithe
8	1815	98.6	352	1	CKR5_PYGBI	O97880 pygathrix b
9	1815	98.6	352	1	CKR5_PYGNE	O97882 pygathrix n
10	1814	98.5	352	1	CKR5_HYLLE	O97883 hylobates l
11	1813	98.5	352	1	CKR5_MACMU	P79436 macaca mula
12	1803	97.9	352	1	CKR5_CERTO	O62743 cercocebus
13	1790	97.2	352	1	CKR5_CERAE	P56493 cercopithec
14	1556	84.5	354	1	CKR5_MOUSE	P51682 mus musculu
15	1547	84.0	354	1	CKR5_RAT	O08556 rattus norv
16	1370.5	74.4	373	1	CKR2_MOUSE	P51683 mus musculu
17	1363.5	74.1	373	1	CKR2_RAT	O55193 rattus norv
18	1349	73.3	360	1	CKR2_MACMU	O18793 macaca mula
19	1224	66.5	374	1	CKR2_HUMAN	P41597 homo sapien
20	1055	57.3	355	1	CKR1_HUMAN	P32246 homo sapien
21	1017.5	55.3	359	1	CKR3_MOUSE	P51678 mus musculu
22	1015.5	55.2	359	1	CKR3_RAT	O54814 rattus norv
23	1009	54.8	355	1	CKR1_MACMU	P56482 macaca mula
24	1004.5	54.6	355	1	CKR1_MOUSE	P51675 mus musculu
25	949	51.5	358	1	CKR3_CAVPO	Q9z2i3 cavia porce
26	938.5	51.0	355	1	CKR3_HUMAN	P51677 homo sapien
27	929.5	50.5	355	1	CKR3_MACMU	P56483 macaca mula
28	919	49.9	360	1	CKR4_HUMAN	P51679 homo sapien
29	911.5	49.5	355	1	CKR3_CERAE	P56492 cercopithec
30	906	49.2	360	1	CKR4_MOUSE	P51680 mus musculu
31	799.5	43.4	356	1	CKRV_MOUSE	P51676 mus musculu
32	746.5	40.5	355	1	CKR8_HUMAN	P51685 homo sapien
33	737	40.0	356	1	CKR8_MACMU	O97665 macaca mula
34	734	39.9	353	1	CKR8_MOUSE	P56484 mus musculu
35	712	38.7	354	1	C3X1_RAT	P35411 rattus norv
36	693	37.6	354	1	C3X1_MOUSE	Q9z0d9 mus musculu
37	670.5	36.4	355	1	C3X1_HUMAN	P49238 homo sapien
38	596	32.4	357	1	CKR9_HUMAN	P51686 homo sapien
39	584	31.7	369	1	CKR9_MOUSE	Q9wut7 mus musculu
40	573.5	31.2	378	1	CKD6_MOUSE	O08707 mus musculu
41	572.5	31.1	382	1	CKD6_RAT	O09027 rattus norv
42	569.5	30.9	384	1	CKD6_HUMAN	O00590 homo sapien
43	567	30.8	378	1	CKR7_HUMAN	P32248 homo sapien
44	562	30.5	378	1	CKR7_MOUSE	P47774 mus musculu
45	559	30.4	374	1	CKR6_HUMAN	P51684 homo sapien

ALIGNMENTS

RESULT 1
CKR5_HUMAN
ID CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; Q9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CCR5 OR CMKBR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
RT CC-chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RT RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).

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RN   [6]
RP   SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX   MEDLINE=98022612; PubMed=9359654;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98049523; PubMed=9388201;
RA   Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT   "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT   with 5'-end heterogeneity, dual promoter usage, and evidence for
RT   polymorphisms within the regulatory regions and noncoding exons.";
RL   J. Biol. Chem. 272:30662-30671(1997).
RN   [8]
RP   SEQUENCE FROM N.A., AND VARIANT ARG-178.
RA   Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
RA   Debre P.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX   MEDLINE=96260017; PubMed=8649511;
RA   Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
RA   di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
RA   Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT   "Identification of a major co-receptor for primary isolates of
RT   HIV-1.";
RL   Nature 381:661-666(1996).
RN   [10]
RP   CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX   MEDLINE=96260018; PubMed=8649512;
RA   Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RA   Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
RA   Paxton W.A.;
RT   "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
RT   CC-CKR-5.";
RL   Nature 381:667-673(1996).
RN   [11]
RP   SULFATION.
RX   MEDLINE=99189752; PubMed=10089882;
RA   Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA   Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT   "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT   entry.";
RL   Cell 96:667-676(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC       SYNCYTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC       VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC   -!- PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
CC   -!- PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
CC       GLYCOSYLATION.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X91492; CAA62796.1; -.
DR   EMBL; U54994; AAC50598.1; -.
DR   EMBL; U57840; AAB17071.1; -.
DR   EMBL; U95626; AAB57793.1; -.
DR   EMBL; U83326; AAC51797.1; -.
DR   EMBL; AF011500; AAB65700.1; -.
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DR   EMBL; AF011507; AAB65707.1; -.
DR   EMBL; AF011508; AAB65708.1; -.
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DR   EMBL; AF011519; AAB65719.1; -.
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DR   EMBL; AF011535; AAB65735.1; -.
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DR   EMBL; AF011537; AAB65737.1; -.
DR   EMBL; AF031237; AAB94735.1; -.
DR   EMBL; AF052539; AAD18131.1; -.
DR   Genew; HGNC:1606; CCR5.
DR   MIM; 601373; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW   Polymorphism.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION.
FT   MOD_RES      10     10       SULFATION.
FT   MOD_RES      14     14       SULFATION.
FT   MOD_RES      15     15       SULFATION.
FT   VARIANT      10     10       Y -> D (IN INCCR5-71A).
FT                                /FTId=VAR_003481.
FT   VARIANT      29     29       A -> S (IN DBSNP:1800939).
FT                                /FTId=VAR_011839.
FT   VARIANT      31     31       R -> H (IN INCCR5-72A).
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  Best Local Similarity  100.0%;  Pred. No. 9.6e-92;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 2
CKR5_PANTR
ID   CKR5_PANTR     STANDARD;      PRT;   352 AA.
AC   P56440; O02778;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98022612; PubMed=9359654;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97426118; PubMed=9282822;
RA   Zacharova V., Zachar V., Goustin A.S.;
RT   "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT   HIV type 1 host.";
RL   AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98090115; PubMed=9430250;
RA   Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT   "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL   AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF005663; AAB62557.1; -.
DR   EMBL; U94329; AAB58446.1; -.
DR   EMBL; AF011542; AAB65742.1; -.
DR   EMBL; U97666; AAC51670.1; -.
DR   EMBL; AF011540; AAB65740.1; -.
DR   EMBL; U89797; AAC03717.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN       1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31    58       1 (POTENTIAL).
FT   DOMAIN       59    68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69    89       2 (POTENTIAL).
FT   DOMAIN       90    102      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     103   124      3 (POTENTIAL).
FT   DOMAIN       125   141      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     142   166      4 (POTENTIAL).
FT   DOMAIN       167   198      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     199   218      5 (POTENTIAL).
FT   DOMAIN       219   235      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     236   260      6 (POTENTIAL).
FT   DOMAIN       261   277      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     278   301      7 (POTENTIAL).
FT   DOMAIN       302   352      CYTOPLASMIC (POTENTIAL).
FT   DISULFID     101   178      BY SIMILARITY.
FT   MOD_RES      3     3        SULFATION (BY SIMILARITY).
FT   MOD_RES      10    10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14    14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15    15       SULFATION (BY SIMILARITY).
FT   CARBOHYD     268   268      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     123   123      T -> S (IN REF. 1).
SQ   SEQUENCE   352 AA;  40539 MW;  4A33E698B80FE34C CRC64;

  Query Match           99.7%;  Score 1835;  DB 1;  Length 352;
  Best Local Similarity  99.4%;  Pred. No. 2e-91;
  Matches  350;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 3
CKR5_PONPY
ID   CKR5_PONPY     STANDARD;      PRT;   352 AA.
AC   O97881;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075446; AAD19858.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).

SQ   SEQUENCE   352 AA;  40527 MW;  F4E2F47135AF658A CRC64;

  Query Match             99.4%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   99.1%;  Pred. No. 3.7e-91;
  Matches  349;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 4
CKR5_GORGO
ID   CKR5_GORGO     STANDARD;      PRT;   352 AA.
AC   P56439;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF005659; AAB62553.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
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DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40515 MW;  D0E6FCB9FE5EAC84 CRC64;

  Query Match             99.1%;  Score 1825;  DB 1;  Length 352;
  Best Local Similarity   98.9%;  Pred. No. 6.8e-91;
  Matches  348;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKTNVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 5
CKR5_TRAPH
ID   CKR5_TRAPH     STANDARD;      PRT;   352 AA.
AC   O97879;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Trachypithecus phayrei (Phayre's leaf monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Trachypithecus.
OX   NCBI_TaxID=61618;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075443; AAD19855.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40509 MW;  4366F148D3A5938F CRC64;

  Query Match             98.9%;  Score 1821;  DB 1;  Length 352;
  Best Local Similarity   98.0%;  Pred. No. 1.1e-90;
  Matches  345;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||| ||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||:||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 6
CKR5_PAPHA
ID   CKR5_PAPHA     STANDARD;      PRT;   352 AA.
AC   P56441;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Papio hamadryas (Hamadryas baboon), and
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9557, 9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=P.hamadryas;
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=P.hamadryas;
RX   MEDLINE=99210133; PubMed=10195758;
RA   Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT   "Species-specific changes in the CCR5 gene from African and Asian
RT   nonhuman primates.";
RL   AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=P.anubis;
RA   Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF005658; AAB62552.1; -.
DR   EMBL; AF105287; AAD20556.1; -.
DR   EMBL; AF105288; AAD20557.1; -.
DR   EMBL; AF105289; AAD20558.1; -.
DR   EMBL; AF105290; AAD20559.1; -.
DR   EMBL; AF023452; AAC63830.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
FT   CARBOHYD    268    268       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   352 AA;  40489 MW;  5E1504A9BA1FE8B2 CRC64;

  Query Match             98.6%;  Score 1816;  DB 1;  Length 352;
  Best Local Similarity   98.0%;  Pred. No. 2.1e-90;
  Matches  345;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 7
CKR5_TRAFR
ID   CKR5_TRAFR     STANDARD;      PRT;   352 AA.
AC   O97878;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Trachypithecus.
OX   NCBI_TaxID=54180;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
```

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CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075442; AAD19854.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN       1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    31     58       1 (POTENTIAL).
FT   DOMAIN      59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    69     89       2 (POTENTIAL).
FT   DOMAIN      90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   103    124       3 (POTENTIAL).
FT   DOMAIN     125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   142    166       4 (POTENTIAL).
FT   DOMAIN     167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   199    218       5 (POTENTIAL).
FT   DOMAIN     219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   236    260       6 (POTENTIAL).
FT   DOMAIN     261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   278    301       7 (POTENTIAL).
FT   DOMAIN     302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   101    178       BY SIMILARITY.
FT   MOD_RES      3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES     10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES     14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES     15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40496 MW;  4366F148C255938F CRC64;

  Query Match             98.6%;  Score 1816;  DB 1;  Length 352;
  Best Local Similarity   97.7%;  Pred. No. 2.1e-90;
  Matches  344;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| ||||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQETSVGL 352


RESULT 8
CKR5_PYGBI
ID   CKR5_PYGBI     STANDARD;      PRT;   352 AA.
AC   O97880;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=61621;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075445; AAD19857.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN       1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    31     58       1 (POTENTIAL).
FT   DOMAIN      59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    69     89       2 (POTENTIAL).
FT   DOMAIN      90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   103    124       3 (POTENTIAL).
FT   DOMAIN     125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   142    166       4 (POTENTIAL).
FT   DOMAIN     167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   199    218       5 (POTENTIAL).
FT   DOMAIN     219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   236    260       6 (POTENTIAL).
FT   DOMAIN     261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   278    301       7 (POTENTIAL).
FT   DOMAIN     302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   101    178       BY SIMILARITY.
FT   MOD_RES      3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES     10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES     14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES     15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40585 MW;  4366F142730F938F CRC64;

  Query Match             98.6%;  Score 1815;  DB 1;  Length 352;
  Best Local Similarity   97.7%;  Pred. No. 2.3e-90;
  Matches  344;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| ||||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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                ||||||||:||||||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                |||||||||||||||||||||| ||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCYIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 9
CKR5_PYGNE
ID   CKR5_PYGNE     STANDARD;      PRT;   352 AA.
AC   O97882;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pygathrix nemaeus (Dove langur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=54133;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075448; AAD19860.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN       1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    31     58       1 (POTENTIAL).
FT   DOMAIN      59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    69     89       2 (POTENTIAL).
FT   DOMAIN      90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   103    124       3 (POTENTIAL).
FT   DOMAIN     125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   142    166       4 (POTENTIAL).
FT   DOMAIN     167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   199    218       5 (POTENTIAL).
FT   DOMAIN     219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   236    260       6 (POTENTIAL).
FT   DOMAIN     261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   278    301       7 (POTENTIAL).
FT   DOMAIN     302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   101    178       BY SIMILARITY.
FT   MOD_RES      3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES     10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES     14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES     15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40532 MW;  FE4F9D98D3B3E861 CRC64;

  Query Match             98.6%;  Score 1815;  DB 1;  Length 352;
  Best Local Similarity   97.4%;  Pred. No. 2.3e-90;
  Matches  343;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEHEISVGL 352


RESULT 10
CKR5_HYLLE
ID   CKR5_HYLLE     STANDARD;      PRT;   352 AA.
AC   O97883;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Hylobates leucogenys (White-cheeked gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=61853;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075451; AAD19863.1; -.
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DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40445 MW;  4F8E4F344CEB7C91 CRC64;

  Query Match             98.5%;  Score 1814;  DB 1;  Length 352;
  Best Local Similarity   98.3%;  Pred. No. 2.6e-90;
  Matches  346;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:| |||||||||||||||||||||||||||||||||||:||||||
Db          1 MDYQVSSPTYDIDYDTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILVLINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 11
CKR5_MACMU
ID   CKR5_MACMU     STANDARD;      PRT;   352 AA.
AC   P79436; O02746;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Macaca mulatta (Rhesus macaque),
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544, 9541, 9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta;
RX   MEDLINE=97184592; PubMed=9032394;
RA   Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA   Newman W., Gerard N., Gerard C., Sodroski J.;
RT   "Utilization of C-C chemokine receptor 5 by the envelope
RT   glycoproteins of a pathogenic simian immunodeficiency virus,
RT   SIVmac239.";
RL   J. Virol. 71:2522-2527(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta; STRAIN=Indian macaque;
RX   MEDLINE=97213934; PubMed=9060623;
RA   Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT   "Genetically divergent strains of simian immunodeficiency virus use
RT   CCR5 as a coreceptor for entry.";
RL   J. Virol. 71:2705-2714(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta;
RX   MEDLINE=21354176; PubMed=11461684;
RA   Margulies B.J., Hauer D.A., Clements J.E.;
RT   "Identification and comparison of eleven rhesus macaque chemokine
RT   receptors.";
RL   AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U77672; AAC51109.1; -.
DR   EMBL; U73739; AAC51158.1; -.
DR   EMBL; U96762; AAC34132.1; -.
DR   EMBL; AF005660; AAB62554.1; -.
DR   EMBL; AF005661; AAB62555.1; -.
DR   EMBL; AF005662; AAB62556.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
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```
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
FT   CARBOHYD    268    268       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    241    241       M -> I (IN REF. 3).
FT   CONFLICT    292    292       I -> M (IN REF. 3).
SQ   SEQUENCE   352 AA;  40507 MW;  58B96C85909FACB2 CRC64;

  Query Match             98.5%;  Score 1813;  DB 1;  Length 352;
  Best Local Similarity   97.7%;  Pred. No. 3e-90;
  Matches  344;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:||||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 12
CKR5_CERTO
ID   CKR5_CERTO     STANDARD;      PRT;   352 AA.
AC   O62743; O62744; O62745; O62746;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Isolate 079, 085, 087, and 089;
RX   MEDLINE=98321155; PubMed=9656999;
RA   Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT   "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT   naturally infected in west Africa: a comparison of coreceptor usage
RT   of primary SIVsm, HIV-2, and SIVmac.";
RL   Virology 246:113-124(1998).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF051902; AAC39830.1; -.
DR   EMBL; AF051903; AAC39831.1; -.
DR   EMBL; AF051904; AAC39832.1; -.
DR   EMBL; AF051905; AAC39833.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
FT   VARIANT       2      2       D -> E (IN ISOLATE 087).
FT   VARIANT       3      3       Y -> D (IN ISOLATE 079).
FT   VARIANT      25     25       V -> G (IN ISOLATE 087).
FT   VARIANT     100    100       M -> K (IN ISOLATE 079).
FT   VARIANT     107    107       L -> V (IN ISOLATE 089).
FT   VARIANT     134    134       V -> G (IN ISOLATE 079).
FT   VARIANT     146    146       V -> L (IN ISOLATES 085 AND 089).
FT   VARIANT     340    340       T -> I (IN ISOLATE 079).
SQ   SEQUENCE   352 AA;  40489 MW;  20A196E2D47E49CA CRC64;

  Query Match             97.9%;  Score 1803;  DB 1;  Length 352;
  Best Local Similarity   97.4%;  Pred. No. 1e-89;
  Matches  343;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:||||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSP 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEASERASSVYTRSTGEQEISVGL 352


RESULT 13
CKR5_CERAE
ID   CKR5_CERAE     STANDARD;      PRT;   352 AA.
AC   P56493;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=98001387; PubMed=9343222;
RA   Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT   "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT   implicate specific amino acids in infections by simian and human
RT   immunodeficiency viruses.";
RL   J. Virol. 71:8642-8656(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT   "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT   gene.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U83324; AAC51795.1; -.
DR   EMBL; U83325; AAC51796.1; -.
DR   EMBL; AB015944; BAA31328.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW   Polymorphism.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      31    58       1 (POTENTIAL).
FT   DOMAIN        59    68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      69    89       2 (POTENTIAL).
FT   DOMAIN        90    102      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      103   124      3 (POTENTIAL).
FT   DOMAIN        125   141      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      142   166      4 (POTENTIAL).
FT   DOMAIN        167   198      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      199   218      5 (POTENTIAL).
FT   DOMAIN        219   235      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      236   260      6 (POTENTIAL).
FT   DOMAIN        261   277      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      278   301      7 (POTENTIAL).
FT   DOMAIN        302   352      CYTOPLASMIC (POTENTIAL).
FT   DISULFID      101   178      BY SIMILARITY.
FT   MOD_RES       3     3        SULFATION (BY SIMILARITY).
FT   MOD_RES       10    10       SULFATION (BY SIMILARITY).
FT   MOD_RES       15    15       SULFATION (BY SIMILARITY).
FT   VARIANT       14    14       N -> Y.
FT   VARIANT       352   352      F -> L.
SQ   SEQUENCE   352 AA;  40561 MW;  7F52E690C72EC29A CRC64;

  Query Match             97.2%;  Score 1790;  DB 1;  Length 352;
  Best Local Similarity   97.2%;  Pred. No. 4.9e-89;
  Matches  341;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| ||| : |||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||:|||||||||||||||||||||||||||||||| ||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPRIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVG 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQETSVG 351


RESULT 14
CKR5_MOUSE
ID   CKR5_MOUSE     STANDARD;      PRT;   354 AA.
AC   P51682; Q61867; P97405; O35313; P97308; O35891;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE   alpha receptor).
GN   CCR5 OR CMKBR5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Spleen;
RX   MEDLINE=96205938; PubMed=8631787;
RA   Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA   Charo I.F.;
RT   "Molecular cloning and functional expression of murine JE (monocyte
RT   chemoattractant protein 1) and murine macrophage inflammatory protein
RT   1alpha receptors: evidence for two closely linked C-C chemokine
RT   receptors on chromosome 9.";
RL   J. Biol. Chem. 271:7551-7558(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX   MEDLINE=96278910; PubMed=8662890;
RA   Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT   "Cloning and characterization of a novel murine macrophage
RT   inflammatory protein-1 alpha receptor.";
RL   J. Biol. Chem. 271:14445-14451(1996).
```

```
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Ola;
RA   Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6, and NIH Swiss; TISSUE=Liver, Kidney, and Spleen;
RX   MEDLINE=98001387; PubMed=9343222;
RA   Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT   "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT   implicate specific amino acids in infections by simian and human
RT   immunodeficiency viruses.";
RL   J. Virol. 71:8642-8656(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=97404635; PubMed=9261347;
RA   Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA   Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT   "Two distinct CCR5 domains can mediate coreceptor usage by human
RT   immunodeficiency virus type 1.";
RL   J. Virol. 71:6305-6314(1997).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Guo B., Kuno K., Harada A., Matsushima K.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
CC       BUT NOT IN NONHEMATOPOIETIC CELL LINES.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U47036; AAC52454.1; -.
DR   EMBL; X94151; CAA63867.1; -.
DR   EMBL; U68565; AAB37273.1; -.
DR   EMBL; U83327; AAC53386.1; -.
DR   EMBL; AF022990; AAC53389.1; -.
DR   EMBL; AF019772; AAB71183.1; -.
DR   EMBL; D83648; BAA12024.1; -.
DR   MGD; MGI:107182; Cmkbr5.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      33    60       1 (POTENTIAL).
FT   DOMAIN        61    70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      71    91       2 (POTENTIAL).
FT   DOMAIN        92    104      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      105   126      3 (POTENTIAL).
FT   DOMAIN        127   143      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      144   168      4 (POTENTIAL).
FT   DOMAIN        169   200      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      201   220      5 (POTENTIAL).
FT   DOMAIN        221   237      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      238   262      6 (POTENTIAL).
FT   DOMAIN        263   279      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      280   303      7 (POTENTIAL).
FT   DOMAIN        304   354      CYTOPLASMIC (POTENTIAL).
FT   DISULFID      103   180      BY SIMILARITY.
FT   CARBOHYD      270   270      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT       11    11       I -> S.
FT   VARIANT       62    62       K -> R.
FT   VARIANT       66    66       V -> M.
FT   VARIANT       97    97       I -> V.
FT   VARIANT       109   109      V -> L.
FT   VARIANT       156   156      V -> A.
FT   VARIANT       160   160      F -> S.
FT   VARIANT       185   185      P -> L.
FT   VARIANT       213   213      I -> V.
FT   VARIANT       318   318      I -> M.
FT   VARIANT       337   337      V -> A.
FT   CONFLICT      3     3        F -> L (IN REF. 2).
FT   CONFLICT      80    80       L -> F (IN REF. 2).
FT   CONFLICT      145   145      N -> I (IN REF. 5).
FT   CONFLICT      190   190      H -> Y (IN REF. 3).
FT   CONFLICT      208   208      P -> S (IN REF. 1).
SQ   SEQUENCE   354 AA;  40863 MW;  B4A6B942E88F9CF0 CRC64;

  Query Match             84.5%;  Score 1556;  DB 1;  Length 354;
  Best Local Similarity   81.9%;  Pred. No. 1.3e-76;
  Matches  290;  Conservative   29;  Mismatches   33;  Indels    2;  Gaps    1;

Qy          1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC 58
              ||:| | |  |||| :|  | |||||||||||:||||||||||||||||||:| |||| :|
Db          1 MDFQGSVPTYIYDIDYGMSAPCQKINVKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISC 60

Qy         59 KRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF 118
              |:|||:|||||||||||| |||| :|||||||| :| ||| ||:: ||:| ||:| ||||
Db         61 KKLKSVTDIYLLNLAISDLLFLLTLPFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFF 120

Qy        119 IILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTC 178
              |||||||||||:|||||||| ||| |||:|||:|||||||||||| |||||||||| ||||
Db        121 IILLTIDRYLAIVHAVFALKVRTVNFGVITSVVTWVVAVFASLPEIIFTRSQKEGFHYTC 180

Qy        179 SSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIF 238
              | |||::|| |||:|||||:||| |:|||||:||||||| || ||||||||||||||||
Db        181 SPHFPHTQYHFWKSFQTLKMVILSLILPLLVMIICYSGILHTLFRCRNEKKRHRAVRLIF 240

Qy        239 TIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYA 298
              |||||||| |||||||| ||||||||||||||||||||||| ||||||||||:||:|||
Db        241 AIMIVYFLFWTPYNIVLLLTTFQEFFGLNNCSSSNRLDQAMQATETLGMTHCCLNPVIYA 300

Qy        299 FVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||:|| |||:||| ||||| ||||||: |:| |||||||||| |:| ||
Db        301 FVGEKFRSYLSVFFRKHIVKRFCKRCSIFQQDNPDRVSSVYTRSTGEHEVSTGL 354


RESULT 15
CKR5_RAT
ID   CKR5_RAT       STANDARD;      PRT;   354 AA.
AC   O08556;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE   alpha receptor).
GN   CCR5 OR CMKBR5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=98334064; PubMed=9670989;
RA   Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA   Berger M., Gebicke-Haerter P.J.;
RT   "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
RT   upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL   J. Neurosci. Res. 53:16-28(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
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RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=98318173; PubMed=9655467;
RA   Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA   Deflebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT   "Chemokine receptor expression in cultured glia and rat experimental
RT   allergic encephalomyelitis.";
RL   J. Neuroimmunol. 86:1-12(1998).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y12009; CAA72737.1; -.
DR   EMBL; U77350; AAC03243.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     33     60       1 (POTENTIAL).
FT   DOMAIN       61     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     91       2 (POTENTIAL).
FT   DOMAIN       92    104       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    105    126       3 (POTENTIAL).
FT   DOMAIN      127    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    168       4 (POTENTIAL).
FT   DOMAIN      169    200       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    201    220       5 (POTENTIAL).
FT   DOMAIN      221    237       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    238    262       6 (POTENTIAL).
FT   DOMAIN      263    279       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    280    303       7 (POTENTIAL).
FT   DOMAIN      304    354       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    103    180       BY SIMILARITY.
FT   CARBOHYD    270    270       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   354 AA;  41030 MW;  77EDB368AA4C868D CRC64;

  Query Match            84.0%;  Score 1547;  DB 1;  Length 354;
  Best Local Similarity  81.9%;  Pred. No. 4e-76;
  Matches  290;  Conservative   27;  Mismatches   35;  Indels    2;  Gaps    1;

Qy          1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC 58
              ||:| | |  ||||:|  | ||||:|||||||:|||||||||||||||||:| ||||:|
Db          1 MDFQGSIPTYIYDIDYSMSAPCQKVNVKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISC 60

Qy         59 KRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF 118
              |:||||||||| |||||| ||||:|||||||| :| ||| ||:| ||:| ||:| ||||
Db         61 KKLKSMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGIYHIGYFGGIFF 120

Qy        119 IILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTC 178
              |||||||||||:||||||:|||||  |||:|||:|||||||  ||| |||  |||||  ||||
Db        121 IILLTIDRYLAIVHAVFAIKARTVNFGVITSVVTWVVAVFVSLPEIIFMRSQKEGSHYTC 180

Qy        179 SSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIF 238
              | || : ||:|||:|||||:||| |:|||||||||||||  || ||||||||||||||||
Db        181 SPHFLHIQYRFWKHFQTLKMVILSLILPLLVMVICYSGILNTLFRCRNEKKRHRAVRLIF 240

Qy        239 TIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYA 298
              |||||||||  |||||||  ||||:||||||||||||||||||||||||:||:|||
Db        241 AIMIVYFLFWTPYNIVLLLTTFQEYFGLNNCSSSNRLDQAMQVTETLGMTHCCLNPVIYA 300

Qy        299 FVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                  ||||||||||  |||:|||  |||||  ||||  |:| ||||||||||||:| ||
Db        301 FVGEKFRNYLSVFFRKHIVKRFCKHCSIFQQVNPDRVSSVYTRSTGEQEVSTGL 354

Search completed: June  3, 2003, 15:19:38
Job time : 21.1411 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:14:58 ; Search time 73.8765 Seconds
(without alignments)
981.754 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1825	99.1	352	6	Q95NC5	Q95nc5 hylobates s
2	1823	99.0	352	6	O18771	O18771 pan troglod
3	1823	99.0	352	6	O18772	O18772 pan troglod
4	1822	99.0	352	6	Q9XS99	Q9xs99 gorilla gor
5	1821	98.9	352	6	Q9TV50	Q9tv50 pan troglod
6	1818	98.8	352	6	Q95NC0	Q95nc0 hylobates m
7	1817	98.7	352	6	Q95NC7	Q95nc7 nasalis lar
8	1816	98.6	352	6	Q95NC8	Q95nc8 colobus pol
9	1813	98.5	352	6	O97962	O97962 pygathrix a
10	1812	98.4	352	6	Q9XT14	Q9xt14 colobus gue
11	1812	98.4	352	6	Q95NC1	Q95nc1 theropithec
12	1811	98.4	352	6	Q95NC6	Q95nc6 trachypithe
13	1811	98.4	352	6	Q95NC3	Q95nc3 miopithecus
14	1809	98.3	352	6	Q9XT13	Q9xt13 papio anubi
15	1808	98.2	352	6	O18770	O18770 pan troglod
16	1808	98.2	352	6	Q9TSK1	Q9tsk1 cercopithec
17	1808	98.2	352	6	Q9TV49	Q9tv49 cercocebus
18	1807	98.2	352	6	O97975	O97975 macaca arct
19	1806	98.1	352	6	Q9XT12	Q9xt12 cercopithec
20	1803	97.9	352	6	Q9TV42	Q9tv42 cercopithec
21	1803	97.9	352	6	Q95NE8	Q95ne8 cercopithec
22	1803	97.9	352	6	Q95ND2	Q95nd2 mandrillus
23	1802	97.9	352	6	O77776	O77776 cercocebus
24	1802	97.9	352	6	Q9MZA3	Q9mza3 hylobates a
25	1801	97.8	352	6	Q95ND1	Q95nd1 mandrillus
26	1800	97.8	352	6	Q95NE1	Q95ne1 cercocebus
27	1800	97.8	352	6	Q95ND0	Q95nd0 erythrocebu
28	1797	97.6	352	6	Q9TV93	Q9tv93 macaca arct
29	1796	97.6	352	6	Q9TV46	Q9tv46 cercopithec
30	1795	97.5	352	6	Q9TQX0	Q9tqx0 cercopithec
31	1794	97.4	352	6	Q9BGN5	Q9bgn5 cercopithec
32	1794	97.4	352	6	Q9XS35	Q9xs35 macaca neme
33	1791	97.3	352	6	Q9TV43	Q9tv43 cercopithec
34	1789	97.2	352	6	Q9TV47	Q9tv47 cercopithec
35	1789	97.2	352	6	Q9TSQ7	Q9tsq7 cercopithec
36	1787	97.1	352	6	Q9XT76	Q9xt76 cercopithec
37	1786	97.0	352	6	Q9MZA2	Q9mza2 cercopithec
38	1784	96.9	352	6	Q9TV48	Q9tv48 cercopithec
39	1779	96.6	339	4	Q9UBT9	Q9ubt9 homo sapien
40	1779	96.6	352	6	Q9TV44	Q9tv44 cercopithec
41	1776	96.5	339	4	Q9UN27	Q9un27 homo sapien
42	1776	96.5	339	4	Q9UBJ7	Q9ubj7 homo sapien
43	1775	96.4	339	4	Q9UN23	Q9un23 homo sapien
44	1774	96.4	339	4	Q9UN28	Q9un28 homo sapien
45	1774	96.4	352	6	Q9TV45	Q9tv45 cercopithec

ALIGNMENTS

RESULT 1
Q95NC5
ID Q95NC5 PRELIMINARY; PRT; 352 AA.
AC Q95NC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF177884; AAK43367.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 99.1%; Score 1825; DB 6; Length 352;
Best Local Similarity 98.9%; Pred. No. 9.5e-147;
Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 2
O18771
ID   O18771      PRELIMINARY;      PRT;   352 AA.
AC   O18771;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CCR5 receptor (Fragment).
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CHCCR5-141A;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR   EMBL; AF011539; AAB65739.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     352    352
SQ   SEQUENCE   352 AA;  40466 MW;  3FFFAC7ABAE1D4FB CRC64;

  Query Match             99.0%;  Score 1823;  DB 6;  Length 352;
  Best Local Similarity   98.9%;  Pred. No. 1.4e-146;
  Matches  348;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISNLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||:|||||||||||||||||||||||||||||||||||||||| ||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKGGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 3
O18772
ID   O18772      PRELIMINARY;      PRT;   352 AA.
AC   O18772;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CCR5 receptor (Fragment).
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CHCCR5-142A;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR   EMBL; AF011541; AAB65741.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     352    352
SQ   SEQUENCE   352 AA;  40598 MW;  39688FA7004C952F CRC64;

  Query Match             99.0%;  Score 1823;  DB 6;  Length 352;
  Best Local Similarity   98.9%;  Pred. No. 1.4e-146;
  Matches  348;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVDNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYDIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 4
Q9XS99
ID   Q9XS99      PRELIMINARY;      PRT;   352 AA.
AC   Q9XS99;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CC chemokine receptor 5.
GN   CCR5.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GORILLACCR;
RX   MEDLINE=99210133; PubMed=10195758;
RA   Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;
RT   "Species-specific changes in the CCR5 gene from African and Asian
RT   nonhuman primates.";
RL   AIDS Res. Hum. Retroviruses 15:479-483(1999).
DR   EMBL; AF105291; AAD20560.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40529 MW;  1BE68C68FE2E7AD0 CRC64;

  Query Match             99.0%;  Score 1822;  DB 6;  Length 352;
  Best Local Similarity   98.6%;  Pred. No. 1.7e-146;
  Matches  347;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||| |||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKTNVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||:|||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGLVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 5
Q9TV50
ID   Q9TV50      PRELIMINARY;      PRT;   352 AA.
AC   Q9TV50;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CC chemokine receptor type 5.
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1410;
RX   MEDLINE=99335215; PubMed=10408730;
RA   Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA   Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT   "Mutations in CCR5-coding sequences are not associated with SIV
RT   carrier status in African nonhuman primates.";
RL   AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1410;
RA   Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA   Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF035214; AAD44007.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40481 MW;  2578A0F2C07A4A65 CRC64;

  Query Match             98.9%;  Score 1821;  DB 6;  Length 352;
  Best Local Similarity   98.3%;  Pred. No. 2.1e-146;
  Matches  346;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||:||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 6
Q95NC0
ID   Q95NC0      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Hylobates moloch (silvery gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=81572;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177899; AAK43382.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40436 MW;  9623CA98340CF274 CRC64;

  Query Match             98.8%;  Score 1818;  DB 6;  Length 352;
  Best Local Similarity   98.6%;  Pred. No. 3.7e-146;
  Matches  347;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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                ||||||||| |||:|||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSGPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
               |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
               |||||||||||||||| ||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 7
Q95NC7
ID   Q95NC7      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Nasalis larvatus (Proboscis monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Nasalis.
OX   NCBI_TaxID=43780;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177882; AAK43365.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40537 MW;  51F6F1486E35938E CRC64;

  Query Match             98.7%;  Score 1817;  DB 6;  Length 352;
  Best Local Similarity   97.7%;  Pred. No. 4.5e-146;
  Matches  344;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||| |||||||||||||||||||||||:|||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
               ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAARWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
               |||||||||:|||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
               |||||||||||||||| ||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 8
Q95NC8
ID   Q95NC8      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Colobus polykomos.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Colobus.
OX   NCBI_TaxID=9572;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177881; AAK43364.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40578 MW;  4366F149C3B4938F CRC64;

  Query Match             98.6%;  Score 1816;  DB 6;  Length 352;
  Best Local Similarity   97.7%;  Pred. No. 5.5e-146;
  Matches  344;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
               |||||||||:|||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
               |||||||||||||||| ||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 9
O97962
ID   O97962      PRELIMINARY;   PRT;   352 AA.
AC   O97962;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   C-C chemokine receptor type 5.
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GN   CCR5.
OS   Pygathrix avunculus (Tonkin snub-nosed monkey), and
OS   Pygathrix roxellana (golden snub-nosed monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=66062, 61622;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y.-W., Zhang Y.-P.;
RT   "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF075447; AAD19859.1; -.
DR   EMBL; AF075444; AAD19856.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40482 MW;  037CFA9E12E532F3 CRC64;

  Query Match             98.5%;  Score 1813;  DB 6;  Length 352;
  Best Local Similarity   97.4%;  Pred. No. 9.8e-146;
  Matches  343;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||:||:||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGVHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQETSVGL 352


RESULT 10
Q9XT14
ID   Q9XT14      PRELIMINARY;      PRT;   352 AA.
AC   Q9XT14;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CC chemokine receptor 5.
GN   CCR5.
OS   Colobus guereza (Black-and-white colobus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Colobus.
OX   NCBI_TaxID=33548;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spearman P.W., Mburu D.N., Graham B.S.;
RT   "Differential Utilization of CCR5 Molecules from Three East African
RT   Simian Species by the HIV-1 Envelope Glycoprotein.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF141639; AAD32684.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40550 MW;  9B078EF04D34DB36 CRC64;

  Query Match             98.4%;  Score 1812;  DB 6;  Length 352;
  Best Local Similarity   97.4%;  Pred. No. 1.2e-145;
  Matches  343;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||:||:||||||
Db        121 LLTIDRYLAIVHAVFALKARTATFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCRIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCRIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 11
Q95NC1
ID   Q95NC1      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Theropithecus gelada (Gelada baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Theropithecus.
OX   NCBI_TaxID=9565;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177891; AAK43374.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40475 MW;  4D3643B6C13E90D5 CRC64;

  Query Match             98.4%;  Score 1812;  DB 6;  Length 352;
  Best Local Similarity   97.7%;  Pred. No. 1.2e-145;
  Matches  344;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||||||||||. |||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAGRLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy         121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                |||||||||:|||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db         121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy         181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy         241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy         301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 12
Q95NC6
ID   Q95NC6      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Trachypithecus johnii (hooded leaf monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Trachypithecus.
OX   NCBI_TaxID=66063;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177883; AAK43366.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40462 MW;  52824E0322559F7F CRC64;

  Query Match             98.4%;  Score 1811;  DB 6;  Length 352;
  Best Local Similarity   97.4%;  Pred. No. 1.5e-145;
  Matches  343;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db           1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy         121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Qy         181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRSEKKRHRAVRLIFTI 240
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Qy         301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 13
Q95NC3
ID   Q95NC3      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Miopithecus.
OX   NCBI_TaxID=36231;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177886; AAK43369.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40546 MW;  6464152F3E566AE5 CRC64;

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  Best Local Similarity   97.7%;  Pred. No. 1.5e-145;
  Matches  344;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

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Db           1 MDYQVSSPTYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

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Db         181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy         241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy         301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db         301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSMGEQEISVGL 352


RESULT 14
Q9XT13
ID   Q9XT13      PRELIMINARY;      PRT;   352 AA.
AC   Q9XT13;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CC chemokine receptor 5.
GN   CCR5.
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spearman P.W., Mburu D.N., Graham B.S.;
RT   "Differential Utilization of CCR5 Molecules from Three East African
RT   Simian Species by the HIV-1 Envelope Glycoprotein.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF141640; AAD32685.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40489 MW;  0B47E337C11E2E1E CRC64;

  Query Match             98.3%;  Score 1809;  DB 6;  Length 352;
  Best Local Similarity   97.7%;  Pred. No. 2.1e-145;
  Matches  344;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 15
O18770
ID   O18770      PRELIMINARY;      PRT;   352 AA.
AC   O18770;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CCR5 receptor (Fragment).
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MACCR5-140A;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR   EMBL; AF011538; AAB65738.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     352    352
SQ   SEQUENCE   352 AA;  40523 MW;  4513DB983A28ACB2 CRC64;

  Query Match             98.2%;  Score 1808;  DB 6;  Length 352;
  Best Local Similarity   97.4%;  Pred. No. 2.6e-145;
  Matches  343;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Search completed: June  3, 2003, 15:21:41
Job time : 75.8765 secs
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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:21:53 ; Search time 36.6279 Seconds
(without alignments)
972.777 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	100.0	352	9	US-10-086-814-1	Sequence 1, Appli
2	1841	100.0	352	9	US-09-734-221A-14	Sequence 14, Appl
3	1841	100.0	352	10	US-09-759-841-2	Sequence 2, Appli
4	1841	100.0	352	10	US-09-813-653-15	Sequence 15, Appl
5	1841	100.0	352	10	US-09-796-202-1	Sequence 1, Appli
6	1841	100.0	352	10	US-09-938-719-5	Sequence 5, Appli
7	1841	100.0	352	10	US-09-939-226-5	Sequence 5, Appli
8	1841	100.0	352	10	US-09-938-703-5	Sequence 5, Appli
9	1841	100.0	352	12	US-10-106-623-2	Sequence 2, Appli
10	1835	99.7	352	10	US-09-813-653-17	Sequence 17, Appl
11	1833	99.6	352	9	US-10-232-686-2	Sequence 2, Appli
12	1833	99.6	352	10	US-09-725-285-2	Sequence 2, Appli
13	1833	99.6	352	10	US-09-779-879A-22	Sequence 22, Appl
14	1833	99.6	352	10	US-09-779-880A-22	Sequence 22, Appl
15	1833	99.6	352	10	US-09-195-662A-2	Sequence 2, Appli
16	1833	99.6	352	10	US-09-339-912A-2	Sequence 2, Appli
17	1833	99.6	352	10	US-09-502-783A-2	Sequence 2, Appli
18	1826	99.2	352	10	US-09-779-879A-2	Sequence 2, Appli
19	1826	99.2	352	10	US-09-779-880A-2	Sequence 2, Appli
20	1807	98.2	352	12	US-10-106-623-20	Sequence 20, Appl
21	1365	74.1	360	10	US-09-131-827A-20	Sequence 20, Appl
22	1364	74.1	347	10	US-09-104-792-3	Sequence 3, Appli
23	1364	74.1	360	10	US-09-131-827A-2	Sequence 2, Appli
24	1350	73.3	360	10	US-09-938-719-7	Sequence 7, Appli
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36	1055	57.3	375	9	US-10-219-834-78	Sequence 78, Appl
37	1028	55.8	355	10	US-09-938-719-9	Sequence 9, Appli
38	1028	55.8	355	10	US-09-939-226-9	Sequence 9, Appli
39	1028	55.8	355	10	US-09-938-703-9	Sequence 9, Appli
40	958	52.0	184	10	US-09-938-719-4	Sequence 4, Appli
41	958	52.0	184	10	US-09-939-226-4	Sequence 4, Appli
42	958	52.0	184	10	US-09-938-703-4	Sequence 4, Appli
43	958	52.0	215	10	US-09-938-719-6	Sequence 6, Appli
44	958	52.0	215	10	US-09-939-226-6	Sequence 6, Appli
45	958	52.0	215	10	US-09-938-703-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 1841; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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RESULT 2
US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
;   GENERAL INFORMATION:
;        APPLICANT: LITTMAN, DAN R.
;                   DENG, HONGKUI
;                   ELLMEIER, WILFRIED
;                   LANDAU, NATHANIEL R.
;                   LIU, RONG
;        TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
;                            MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: David A. Jackson, Esq.
;             STREET: 411 Hackensack Ave, Continental Plaza, 4th
;                     Floor
;             CITY: Hackensack
;             STATE: New Jersey
;             COUNTRY: USA
;             ZIP: 07601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/734,221A
;             FILING DATE: 11-Dec-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/666,020
;             FILING DATE: 19-JUN-1996
;             APPLICATION NUMBER: US 08/227,319
;             FILING DATE: 13-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jackson Esq., David A.
;             REGISTRATION NUMBER: 26,742
;             REFERENCE/DOCKET NUMBER: 1049-1-004 N2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 201-487-5800
;             TELEFAX: 201-343-1684
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 352 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        HYPOTHETICAL: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Homo sapiens
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

  Query Match           100.0%;  Score 1841;  DB 9;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-150;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 3
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
;  APPLICANT:  Rickett, Graham A
;  APPLICANT:  Dobbs, Susan
;  APPLICANT:  Perros, Manoussos
;  TITLE OF INVENTION:  Assay Method
;  FILE REFERENCE:  PC10348APME
;  CURRENT APPLICATION NUMBER: US/09/759,841
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER:  GB 0000661.9
;  PRIOR FILING DATE:  2000-01-12
;  PRIOR APPLICATION NUMBER:  GB 0000663.5
;  PRIOR FILING DATE:  2000-01-12
;  PRIOR APPLICATION NUMBER:  GB 0000659.3
;  PRIOR FILING DATE:  2000-01-12
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-759-841-2

  Query Match           100.0%;  Score 1841;  DB 10;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-150;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 4
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
;  APPLICANT: Nestor, John
;  APPLICANT:  Wilson, Carol
;  APPLICANT:  See, Raymond
;  APPLICANT:  Tan Hehir, Christina
;  TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
;  FILE REFERENCE: CNS-005
;  CURRENT APPLICATION NUMBER: US/09/813,653
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/190,946
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/190,996
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/191,299
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-653-15

  Query Match            100.0%;  Score 1841;  DB 10;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-150;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 5
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
;  APPLICANT: Dragic, Tatjana
;  APPLICANT:  Olson, William
;  TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE: 2048/61010/JPW/SHS
;  CURRENT APPLICATION NUMBER: US/09/796,202
;  CURRENT FILING DATE:  2001-02-28
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: human
US-09-796-202-1

  Query Match            100.0%;  Score 1841;  DB 10;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-150;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 6
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
;  GENERAL INFORMATION:
;       APPLICANT: SAMSON, MICHEL
;                  PARMENTIER, MARC
;                  VASSART, GILBERT
;                  LIBERT, FREDERICK
;       TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                           AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive  16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/938,719
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/626,939
;            FILING DATE: 27-JULY-2000
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Altman, Daniel E
;            REGISTRATION NUMBER: 34,115
;            REFERENCE/DOCKET NUMBER: <Unknown>
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 352 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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US-09-938-719-5

Query Match 100.0%; Score 1841; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 7
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-939-226-5

Query Match 100.0%; Score 1841; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 8
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-938-703-5

Query Match 100.0%; Score 1841; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 9
US-10-106-623-2
; Sequence 2, Application US/10106623
; Patent No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Schweickart, Vicky L.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 1841; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 10
US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compound
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 99.7%; Score 1835; DB 10; Length 352;
Best Local Similarity 99.7%; Pred. No. 5.8e-150;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILIQINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 11
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Yi
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000N
;  CURRENT APPLICATION NUMBER: US/10/232,686
;  CURRENT FILING DATE:  2002-09-03
;  PRIOR APPLICATION NUMBER: 09/339,912
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 09/195,662
;  PRIOR FILING DATE: 1998-11-18
;  PRIOR APPLICATION NUMBER: 08/466,343
;  PRIOR FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-232-686-2

  Query Match             99.6%;  Score 1833;  DB 9;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-150;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTEEQEISVGL 352


RESULT 12
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
;  APPLICANT:   Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION:   Antibodies to Human G-Protein Chemokine Receptor HDGNR10
;  TITLE OF INVENTION:  (CCR5 Receptor)
;  FILE REFERENCE:   1488.1150003
;  CURRENT APPLICATION NUMBER: US/09/725,285
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER:   09/339,912
;  PRIOR FILING DATE:   1999-06-25
;  PRIOR APPLICATION NUMBER:   09/195,662
;  PRIOR FILING DATE:   1998-11-18
;  PRIOR APPLICATION NUMBER:   08/466,343
;  PRIOR FILING DATE:   1995-06-06
;  NUMBER OF SEQ ID NOS:   9
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence: Genomic
;   FEATURE:
;   OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

  Query Match             99.6%;  Score 1833;  DB 10;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-150;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTEEQEISVGL 352


RESULT 13
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig A.
;  APPLICANT:  Roschke, Viktor
;  APPLICANT:  Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000A
;  CURRENT APPLICATION NUMBER: US/09/779,879A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,258
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 60/187,999
;  PRIOR FILING DATE: 2000-03-09
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;  PRIOR APPLICATION NUMBER: US 60/234,336
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-779-879A-22

  Query Match             99.6%;  Score 1833;  DB 10;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-150;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTEEQEISVGL 352


RESULT 14
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig A.
;  APPLICANT:  Roschke, Viktor
;  APPLICANT:  Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000C
;  CURRENT APPLICATION NUMBER: US/09/779,880A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,258
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 60/187,999
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: US 60/234,336
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-779-880A-22

  Query Match             99.6%;  Score 1833;  DB 10;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-150;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTEEQEISVGL 352


RESULT 15
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
;  APPLICANT:   Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION:   Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
;  FILE REFERENCE:   1488.1150002
;  CURRENT APPLICATION NUMBER: US/09/195,662A
;  CURRENT FILING DATE:  1998-11-18
;  PRIOR APPLICATION NUMBER:   08/466,343
;  PRIOR FILING DATE:   1995-06-06
;  NUMBER OF SEQ ID NOS:   9
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence: Genomic
;   FEATURE:
;   OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

  Query Match             99.6%;  Score 1833;  DB 10;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-150;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Job time : 46.6279 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:21:53 ; Search time 22.3721 Seconds
(without alignments)
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Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1122	100.0	215	10	US-09-938-719-6	Sequence 6, Appli
2	1122	100.0	215	10	US-09-939-226-6	Sequence 6, Appli
3	1122	100.0	215	10	US-09-938-703-6	Sequence 6, Appli
4	958	85.4	184	10	US-09-938-719-4	Sequence 4, Appli
5	958	85.4	184	10	US-09-939-226-4	Sequence 4, Appli
6	958	85.4	184	10	US-09-938-703-4	Sequence 4, Appli
7	958	85.4	352	9	US-10-232-686-2	Sequence 2, Appli
8	958	85.4	352	9	US-10-086-814-1	Sequence 1, Appli
9	958	85.4	352	9	US-09-734-221A-14	Sequence 14, Appl
10	958	85.4	352	10	US-09-725-285-2	Sequence 2, Appli
11	958	85.4	352	10	US-09-759-841-2	Sequence 2, Appli
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13	958	85.4	352	10	US-09-779-880A-22	Sequence 22, Appl
14	958	85.4	352	10	US-09-813-653-15	Sequence 15, Appl
15	958	85.4	352	10	US-09-796-202-1	Sequence 1, Appli
16	958	85.4	352	10	US-09-195-662A-2	Sequence 2, Appli
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19	958	85.4	352	10	US-09-939-226-5	Sequence 5, Appli
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ALIGNMENTS

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RESULT 1
US-09-938-719-6
; Sequence 6, Application US/09938719
; Patent No. US20020106742A1
;  GENERAL INFORMATION:
;       APPLICANT: SAMSON, MICHEL
;                  PARMENTIER, MARC
;                  VASSART, GILBERT
;                  LIBERT, FREDERICK
;       TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                           AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive  16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/938,719
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/626,939
;            FILING DATE: 27-JULY-2000
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Altman, Daniel E
;            REGISTRATION NUMBER: 34,115
;            REFERENCE/DOCKET NUMBER: <Unknown>
;  INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 215 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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US-09-938-719-6

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  Best Local Similarity   100.0%;  Pred. No. 4.2e-104;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
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; Sequence 6, Application US/09939226
; Patent No. US20020110805A1
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/939,226
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 2000-07-27
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;    INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 215 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6

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  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-09-938-703-6
; Sequence 6, Application US/09938703
; Patent No. US20020110870A1
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/938,703
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 2000-07-27
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;    INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 215 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

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RESULT 4
US-09-938-719-4
; Sequence 4, Application US/09938719
; Patent No. US20020106742A1
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/938,719
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 27-JULY-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 184 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4

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  Best Local Similarity   100.0%;  Pred. No. 7.5e-88;
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RESULT 5
US-09-939-226-4
; Sequence 4, Application US/09939226
; Patent No. US20020110805A1
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/939,226
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 2000-07-27
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 184 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4

  Query Match             85.4%;  Score 958;  DB 10;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        181 HFPY 184


RESULT 6
US-09-938-703-4
; Sequence 4, Application US/09938703
; Patent No. US20020110870A1
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
```

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;       TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                           AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive  16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/938,703
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/626,939
;            FILING DATE: 2000-07-27
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Altman, Daniel E
;            REGISTRATION NUMBER: 34,115
;            REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 184 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

  Query Match             85.4%;  Score 958;  DB 10;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 7
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Yi
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000N
;  CURRENT APPLICATION NUMBER: US/10/232,686
;  CURRENT FILING DATE:  2002-09-03
;  PRIOR APPLICATION NUMBER: 09/339,912
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 09/195,662
;  PRIOR FILING DATE: 1998-11-18
;  PRIOR APPLICATION NUMBER: 08/466,343
;  PRIOR FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-232-686-2

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  Best Local Similarity   100.0%;  Pred. No. 1.6e-87;
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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 8
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
;  APPLICANT: Dragic, Tatjana
;  APPLICANT:  Olson, Wlliam C.
;  TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE: 61010-AB-1
;  CURRENT APPLICATION NUMBER: US/10/086,814
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-086-814-1

  Query Match             85.4%;  Score 958;  DB 9;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 9
US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
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;  GENERAL INFORMATION:
;       APPLICANT: LITTMAN, DAN R.
;                  DENG, HONGKUI
;                  ELLMEIER, WILFRIED
;                  LANDAU, NATHANIEL R.
;                  LIU, RONG
;       TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
;                           MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
;                           USES THEREOF
;       NUMBER OF SEQUENCES: 14
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: David A. Jackson, Esq.
;            STREET: 411 Hackensack Ave, Continental Plaza, 4th
;                    Floor
;            CITY: Hackensack
;            STATE: New Jersey
;            COUNTRY: USA
;            ZIP: 07601
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/734,221A
;            FILING DATE: 11-Dec-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/666,020
;            FILING DATE: 19-JUN-1996
;            APPLICATION NUMBER: US 08/227,319
;            FILING DATE: 13-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Jackson Esq., David A.
;            REGISTRATION NUMBER: 26,742
;            REFERENCE/DOCKET NUMBER: 1049-1-004 N2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 201-487-5800
;            TELEFAX: 201-343-1684
;  INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 352 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Homo sapiens
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 10
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
;  APPLICANT:   Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION:   Antibodies to Human G-Protein Chemokine Receptor HDGNR10
;  TITLE OF INVENTION:  (CCR5 Receptor)
;  FILE REFERENCE:   1488.1150003
;  CURRENT APPLICATION NUMBER: US/09/725,285
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER:   09/339,912
;  PRIOR FILING DATE:   1999-06-25
;  PRIOR APPLICATION NUMBER:   09/195,662
;  PRIOR FILING DATE:   1998-11-18
;  PRIOR APPLICATION NUMBER:   08/466,343
;  PRIOR FILING DATE:   1995-06-06
;  NUMBER OF SEQ ID NOS:   9
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence: Genomic
;   FEATURE:
;   OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 11
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
;  APPLICANT:  Rickett, Graham A
;  APPLICANT:  Dobbs, Susan
;  APPLICANT:  Perros, Manoussos
;  TITLE OF INVENTION:  Assay Method
;  FILE REFERENCE:  PC10348APME
;  CURRENT APPLICATION NUMBER: US/09/759,841
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER:  GB 0000661.9
;  PRIOR FILING DATE:  2000-01-12
;  PRIOR APPLICATION NUMBER:  GB 0000663.5
;  PRIOR FILING DATE:  2000-01-12
;  PRIOR APPLICATION NUMBER:  GB 0000659.3
;  PRIOR FILING DATE:  2000-01-12
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-09-759-841-2

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 12
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig A.
;  APPLICANT:  Roschke, Viktor
;  APPLICANT:  Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000A
;  CURRENT APPLICATION NUMBER: US/09/779,879A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,258
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 60/187,999
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: US 60/234,336
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-779-879A-22

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Qy        181 HFPY 184
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RESULT 13
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig A.
;  APPLICANT:  Roschke, Viktor
;  APPLICANT:  Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000C
;  CURRENT APPLICATION NUMBER: US/09/779,880A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,258
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 60/187,999
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: US 60/234,336
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 58
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;   ORGANISM: Homo sapiens
US-09-779-880A-22

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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 14
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
;  APPLICANT: Nestor, John
;  APPLICANT:  Wilson, Carol
;  APPLICANT:  See, Raymond
;  APPLICANT:  Tan Hehir, Christina
;  TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compound
;  FILE REFERENCE: CNS-005
;  CURRENT APPLICATION NUMBER: US/09/813,653
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/190,946
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/190,996
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/191,299
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
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US-09-813-653-15
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  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 15
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
;  APPLICANT: Dragic, Tatjana
;  APPLICANT:  Olson, William
;  TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE: 2048/61010/JPW/SHS
;  CURRENT APPLICATION NUMBER: US/09/796,202
;  CURRENT FILING DATE:  2001-02-28
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: human
US-09-796-202-1

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Db        181 HFPY 184


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GenCore version 5.1.6

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1122	100.0	215	20	AAW88238	HIV-1 co-receptor
3	958	85.4	184	18	AAW27406	Inactive human CCR
4	958	85.4	352	18	AAW27407	Human CCR5. Homo
5	958	85.4	352	18	AAW27123	Human chemokine re
6	958	85.4	352	19	AAW23835	Human CC chemokine
7	958	85.4	352	20	AAW88232	HIV-1 co-receptor
8	958	85.4	352	22	ABB56342	Non-endogenous hum
9	958	85.4	352	22	AAG80111	Human CCR5 protein
10	958	85.4	352	22	AAB82948	Human HIV-1 co-rec
11	958	85.4	352	22	AAE07039	Human G-protein ch
12	958	85.4	352	22	AAE07048	Human G-protein ch
13	958	85.4	352	22	AAB83354	Human CCR5 protein
14	958	85.4	352	22	AAE04321	Human chemokine re
15	958	85.4	352	22	AAB46858	Human HDGNR10 prot
16	958	85.4	352	23	AAU97152	Human G-protein ch
17	958	85.4	352	23	ABB08343	Human chemokine (C
18	958	85.4	352	23	AAM52828	Human CC chemokine
19	958	85.4	439	20	AAY41280	Fusion protein con
20	953	84.9	371	19	AAW23834	Human CC chemokine
21	952	84.8	352	23	AAM52829	Human CCR5 Gln 55
22	943	84.0	352	18	AAW07602	Human G-protein ch
23	943	84.0	352	21	AAY80128	Human G-protein ch
24	943	84.0	352	22	AAE07037	Human G-protein ch
25	943	84.0	352	22	AAE07046	Human G-protein ch
26	943	84.0	352	23	AAU97150	Human G-protein ch
27	936	83.4	352	22	AAG79089	Amino acid sequenc
28	933	83.2	352	18	AAW27125	Macaque chemokine
29	839	74.8	332	18	AAW26766	Human chemokine re
30	776	69.2	354	19	AAW54037	Mouse CC-CKR5 prot
31	695	61.9	360	22	AAU07613	Human CCR2-64I pol
32	694	61.9	360	16	AAR79166	Human monocyte che
33	694	61.9	360	18	AAW35833	Human monocyte che
34	694	61.9	360	22	ABB56340	Non-endogenous hum
35	694	61.9	360	22	AAG80108	Human CCR2b protei
36	694	61.9	360	22	AAU07614	Human wild-type CC
37	694	61.9	374	16	AAR79165	Human monocyte che
38	694	61.9	374	22	AAG80107	Human CCR2a protei
39	608.5	54.2	329	22	AAB46859	Human MCP-1 recept
40	598	53.3	355	15	AAR52749	C-C chemokine rece
41	598	53.3	355	18	AAW26588	Human MIP-1 alpha/
42	598	53.3	355	18	AAW25751	Human MIP-1alpha/R
43	598	53.3	355	21	AAB20571	Human CC-chemokine
44	565.5	50.4	355	18	AAW29179	Rat CC chemokine r
45	547.5	48.8	360	17	AAR99274	Chemokine receptor

ALIGNMENTS

RESULT 1
AAW27408
ID AAW27408 standard; Protein; 215 AA.
XX
AC AAW27408;
XX
DT 14-APR-1998 (first entry)
XX
DE Inactive human CCR5.
XX
KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW predisposition; resistance; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder.
XX
OS Homo sapiens.
XX
PN WO9732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE00023.
XX
PR 06-AUG-1996; 96EP-0870102.
PR 01-MAR-1996; 96EP-0870021.
XX
PA (EURO-) EUROSCREEN SA.
XX
PI Libert F, Parmentier M, Samson M, Vassart G;
XX
DR WPI; 1997-479829/44.

DR N-PSDB; AAT90118.
XX
PT Active and inactive forms of human CC chemokine receptor CCR-5 -
PT useful to diagnose, prevent and/or treat inflammatory disorders,
PT autoimmune disease and viral infection
XX
PS Claim 7; Fig 1d-e; 94pp; English.
XX
CC The present sequence is an inactive human CC (Cys-Cys)
CC chemokine receptor 5 (CCR5), which lacks the last 3 transmembrane
CC regions and the regions involved in G protein-coupling. CCR5 or
CC its cDNA can used to diagnose, treat and/or prevent inflammatory
CC diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma,
CC idiopathic pulmonary fibrosis and psoriasis, viral infections,
CC especially human immunodeficiency virus type 1 or type 2 (HIV-1 or
CC HIV-2) infection, cancer, atherosclerosis and autoimmune disorders.
CC Subjects that express the inactive receptor have a predisposition,
CC or resistance to HIV-1 and/or HIV-2.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1122; DB 18; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
```

RESULT 2
AAW88238
ID AAW88238 standard; Protein; 215 AA.
XX
AC AAW88238;
XX
DT 15-MAR-1999 (first entry)
XX
DE HIV-1 co-receptor CCR5 variant CCR5-delta32.
XX
KW HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Domain	32..56
FT		/note= "transmembrane domain 1"
FT	Domain	67..87
FT		/note= "transmembrane domain 2"
FT	Domain	103..124
FT		/note= "transmembrane domain 3"
FT	Domain	142..167
FT		/note= "transmembrane domain 4"

XX
PN WO9854317-A1.
XX
PD 03-DEC-1998.
XX
PF 29-MAY-1998; 98WO-EP03437.
XX
PR 30-MAY-1997; 97US-0048057.
XX
PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
PI Arenzana Siesdedos F, Beretta A, Braun J, Quillent C;
XX
DR WPI; 1999-059835/05.
DR N-PSDB; AAV84159.
XX
PT New CCR5 variant protein of the HIV-1 co-receptor - useful in
PT developing resistance of CCR5-expressing cells to HIV-1 infection
XX
PS Disclosure; Page 38-39; 55pp; English.
XX
CC This is the amino acid sequence of a CCR5 variant protein,
CC designated CCR5-delta32, that includes the first 4 transmembrane
CC domains of wild-type CCR5 (see AAW88232), but lacks transmembrane
CC domains 5-7. CCR5 serves as a co-receptor for infection by
CC macrophage-tropic (M-tropic) strains of HIV-1. Individuals
CC homozygous for the CCR5-delta32 mutation are resistant to HIV-1
CC infection, but heterozygous individuals are susceptible. The
CC invention additionally relates to the identification of variant
CC CCR5m303 (see AAW88231), which lacks transmembrane domains 3-7 of
CC CCR5. The detection of CCR5 variants may be used to identify
CC individuals at lower risk of infection relative to the general
CC population who, if infected, may exhibit slower progression to
CC AIDS. Probes and primers (see AAV84127-36) are provided for use in
CC diagnostic methods for detecting the presence of such variants. A
CC method is provided for inhibiting HIV-1 infection of a cell
CC expressing the CCR5 receptor. This involves introducing a nucleic
CC acid encoding a CCR5 variant into the cell, thereby reducing the
CC number of functional CCR5 molecules present on the cell surface.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1122; DB 20; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
```

RESULT 3
AAW27406
ID AAW27406 standard; Protein; 184 AA.
XX
AC AAW27406;
XX
DT 14-APR-1998 (first entry)
XX
DE Inactive human CCR5.
XX
KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW predisposition; resistance; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder.
XX

OS Homo sapiens.
XX
PN WO9732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE00023.
XX
PR 06-AUG-1996; 96EP-0870102.
PR 01-MAR-1996; 96EP-0870021.
XX
PA (EURO-) EUROSCREEN SA.
XX
PI Libert F, Parmentier M, Samson M, Vassart G;
XX
DR WPI; 1997-479829/44.
DR N-PSDB; AAT90116.
XX
PT Active and inactive forms of human CC chemokine receptor CCR-5 -
PT useful to diagnose, prevent and/or treat inflammatory disorders,
PT autoimmune disease and viral infection
XX
PS Claim 1; Fig 1a; 94pp; English.
XX
CC The present sequence is an inactive human CC (Cys-Cys)
CC chemokine receptor 5 (CCR5), which is not a receptor of human
CC immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or
CC its cDNA can used to diagnose, treat and/or prevent inflammatory
CC diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma,
CC idiopathic pulmonary fibrosis and psoriasis, viral infections,
CC especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and
CC autoimmune disorders. Subjects that express the inactive receptor
CC have a predisposition, or resistance to HIV-1 and/or HIV-2.
XX
SQ Sequence 184 AA;

Query Match 85.4%; Score 958; DB 18; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.4e-106;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

RESULT 4
AAW27407
ID AAW27407 standard; Protein; 352 AA.
XX
AC AAW27407;
XX
DT 14-APR-1998 (first entry)
XX
DE Human CCR5.
XX
KW Human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder.

XX
OS Homo sapiens.
XX
PN WO9732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE00023.
XX
PR 06-AUG-1996; 96EP-0870102.
PR 01-MAR-1996; 96EP-0870021.
XX
PA (EURO-) EUROSCREEN SA.
XX
PI Libert F, Parmentier M, Samson M, Vassart G;
XX
DR WPI; 1997-479829/44.
DR N-PSDB; AAT90117.
XX
PT Active and inactive forms of human CC chemokine receptor CCR-5 -
PT useful to diagnose, prevent and/or treat inflammatory disorders,
PT autoimmune disease and viral infection
XX
PS Claim 4; Fig 1b-c; 94pp; English.
XX
CC The present sequence is human CC (Cys-Cys) chemokine receptor
CC 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES
CC chemokines, but not by monocyte chemoattractant protein 1 (MCP-1),
CC MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product
CC alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of
CC human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2).
CC CCR5 or its cDNA can used to diagnose, treat and/or prevent
CC inflammatory diseases, e.g. rheumatoid arthritis,
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection,
CC cancer, atherosclerosis and autoimmune disorders.
XX
SQ Sequence 352 AA;

Query Match 85.4%; Score 958; DB 18; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-105;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

RESULT 5
AAW27123
ID AAW27123 standard; Protein; 352 AA.
XX
AC AAW27123;
XX
DT 14-DEC-1997 (first entry)
XX
DE Human chemokine receptor 88C.
XX
KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;

```
KW   G protein coupled receptor; ligand; modulator; antibody; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..32
FT                   /label= Extracellular_domain
FT   Domain          56..67
FT                   /label= Intracellular_domain
FT   Domain          89..112
FT                   /label= Extracellular_domain
FT   Domain          125..145
FT                   /label= Intracellular_domain
FT   Domain          166..191
FT                   /label= Extracellular_domain
FT   Domain          213..235
FT                   /label= Intracellular_domain
FT   Domain          259..280
FT                   /label= Extracellular_domain
FT   Domain          301..352
FT                   /label= Intracellular_domain
XX
PN   WO9722698-A2.
XX
PD   26-JUN-1997.
XX
PF   20-DEC-1996;    96WO-US20759.
XX
PR   07-JUN-1996;    96US-0661393.
PR   20-DEC-1995;    95US-0575967.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Gray PW,  Raport CJ,  Schweickart VL;
XX
DR   WPI; 1997-341689/31.
DR   N-PSDB; AAT85161.
XX
PT   New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT   to modulate leukocyte trafficking, e.g. for treatment of
PT   inflammation, tumours, viral infections, autoimmune diseases, etc.
XX
PS   Claim 16; Page 47-48; 65pp; English.
XX
CC   This polypeptide sequence comprises novel human chemokine receptor
CC   88C, a G protein coupled receptor that is involved in leukocyte
CC   trafficking.  Its amino sequence was deduced from a cDNA clone
CC   (AAT85161) isolated from a macrophage library.  It shows 62% identity
CC   to CCCKR1.  Chemokine receptor 88-2B (see AAW27124) has also been
CC   identified.  88C and 88-2B receptors and their polypeptide fragments
CC   can be produced in transformed host cells.  The receptors, peptides
CC   comprising one or more of the extracellular or intracellular
CC   domains, and anti-receptor antibodies can be used to modulate
CC   receptor activities, particularly ligand and G protein binding, and
CC   are potentially potentially useful in the treatment of
CC   atheroslerosis, rheumatoid arthritis, tumours, asthma, viral
CC   infection, AIDS, inflammatory conditions, pathological immune
CC   response, abnormal haematopoietic processes etc.
XX
SQ   Sequence   352 AA;

  Query Match          85.4%;  Score 958;  DB 18;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 6
AAW23835
ID   AAW23835 standard; Protein; 352 AA.
XX
AC   AAW23835;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Human CC chemokine receptor 5 (CCR5).
XX
KW   CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW   human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW   transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          29..55
FT                   /label= I
FT                   /note= "transmembrane domain"
FT   Region          109..120
FT                   /note= "extracellular loop-1 (Claim 19)"
FT   Domain          104..126
FT                   /label= III
FT                   /note= "transmembrane domain"
FT   Domain          143..171
FT                   /label= IV
FT                   /note= "transmembrane domain"
FT   Region          187..210
FT                   /note= "extracellular loop-2 (Claim 19)"
FT   Domain          194..219
FT                   /label= V
FT                   /note= "transmembrane domain"
FT   Domain          238..258
FT                   /label= VI
FT                   /note= "transmembrane domain"
FT   Region          261..276
FT                   /note= "extracellular loop-3 (Claim 19)"
FT   Domain          277..300
FT                   /label= VII
FT                   /note= "transmembrane domain"
XX
PN   WO9745543-A2.
XX
PD   04-DEC-1997.
XX
PF   28-MAY-1997;    97WO-US09586.
XX
PR   28-MAY-1996;    96US-0018508.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Alkhatib G,  Berger EA,  Broder CC,  Combadiere C;
PI   Feng Y,  Kennedy PE, Murphy PM;
XX
DR   WPI; 1998-032650/03.
DR   N-PSDB; AAT76920.
XX
PT   CC chemokine receptor 5 polypeptide - used to inhibit membrane
PT   fusion between HIV and a target cell
XX
PS   Claim 68; Fig 1C; 70pp; English.
XX
CC   This protein sequence comprises of a novel human macrophage-selective
```

KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
KW hyper-eosinophilic syndrome; vulnerary.
XX
OS Homo sapiens.
XX
PN US2001000241-A1.
XX
PD 12-APR-2001.
XX
PF 29-NOV-2000; 2000US-0725285.
XX
PR 06-JUN-1995; 95US-0466343.
PR 18-NOV-1998; 98US-0195662.
PR 25-JUN-1999; 99US-0339912.
XX
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Li Y, Ruben SM;
XX
DR WPI; 2001-226317/23.
DR N-PSDB; AAF26390.
XX
PT New human G-protein chemokine receptor polypeptides and
PT polynucleotides, useful for identifying (ant)agonists to the G-protein
PT chemokine receptor -
XX
PS Claim 1a; Page 15; 22pp; English.
XX
CC This invention describes a novel receptor polypeptide (I) selected from
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
CC products of the invention have antiinflammatory, immunomodulatory,
CC anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic,
CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
CC activity and can be used for gene therapy. The G-protein chemokine
CC receptors, HDGNR10, (I) are useful for screening for compounds which
CC activate or inhibit activation of (I). The products of the invention can
CC also be used for stimulating haematopoiesis, wound healing, coagulation,
CC angiogenesis, treating solid tumours, chronic infections, leukemia,
CC T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and
CC stimulating growth factor activity. HDGNR10 is useful for treating
CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
CC reactions, prostaglandin-independent fever, bone marrow failure,
CC silicosis, sarcoidosis, rheumatoid arthritis, shock and
CC hyper-eosinophilic syndrome.
CC (N.B. This record was resubmitted to correct errors in the keyword
CC formatting).
XX
SQ Sequence 352 AA;

Query Match 85.4%; Score 958; DB 22; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-105;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
                  ||||
Db        181 HFPY 184
```

Search completed: June 3, 2003, 15:19:03
Job time : 40.4356 secs

```
DR   WPI; 2001-477088/52.
DR   N-PSDB; AAF87099.
XX
PT   Determining if an agent can modulate CCR5-gp120 interaction, comprises
PT   incubating the agent with CCR5 and gp120 and determining if the agent
PT   modulates the interaction -
XX
PS   Claim 1; Page 110; 113pp; English.
XX
CC   This sequence represents the human CCR5 protein sequence.
CC   The invention relates to a method for determining whether an agent is
CC   capable of modulating the interaction of chemotactic chemokine receptor 5
CC   (CCR5) with gp120, comprising incubating the agent with CCR5 and gp120
CC   and determining whether the agent modulates the interaction, where gp120
CC   is associated with CD4, and where the interaction is a low affinity
CC   binding. The method is used to identify an agent capable of modulating
CC   the interaction of CCR5 with gp120. An agent identified by the method
CC   is used to prepare a pharmaceutical composition for the treatment of a
CC   disease or condition associated with CCR5 and gp120 interaction, to treat
CC   a subject with a disease or condition associated with CCR5 and gp120
CC   interaction, and for preparing a pharmaceutical for treating human
CC   immunodeficiency virus (HIV). It can also be treat anti-inflammatory
CC   diseases. The method is commercially useful, amenable to high throughput
CC   screening, and detects interaction of gp120 with cells expressing only
CC   CCR5.
XX
SQ   Sequence   352 AA;

  Query Match           85.4%;  Score 958;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 14
AAE04321
ID   AAE04321 standard; Protein; 352 AA.
XX
AC   AAE04321;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
XX
KW   Human; transformed mammalian cell; CD4; reporter gene; translocation;
KW   human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
KW   chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
KW   CC-CKR-5; envelope glycoprotein; anti-HIV.
XX
OS   Homo sapiens.
XX
PN   US6258527-B1.
XX
PD   10-JUL-2001.
XX
PF   21-MAY-1997;   97US-0861105.
XX
PR   20-MAY-1996;   96US-0017157.
PR   19-JUN-1996;   96US-0020043.
PR   19-MAY-1997;   97US-0858660.
XX
PA   (AARO-) AARON DIAMOND AIDS RES CENT.
PA   (UYNY ) UNIV NEW YORK STATE.
XX
PI   Littman DR,  Deng H,  Ellmeier W,  Landau NR,  Liu R;
XX
DR   WPI; 2001-417127/44.
DR   N-PSDB; AAD08577.
XX
PT   Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
PT   and HIV LTR for identification of drugs and antibodies for treatment of
PT   HIV -
XX
PS   Disclosure; Column 47-50; 37pp; English.
XX
CC   The present invention relates to a transformed mammalian cell that
CC   contains a gene encoding CD4, a construct encoding a reporter gene under
CC   the regulation of an human immuno deficiency virus (HIV) long terminal
CC   repeat (LTR) and that has been transduced with a vector encoding a
CC   human chemokine receptor (CKR) where the CD4 and the CKR are present on
CC   the cell surface of transformed mammalian cell. The invention is useful
CC   for identifying drugs or antibodies that interfere with the
CC   translocation of HIV into transformed mammalian cell or for identifying
CC   a human chemokine receptor that facilitates the infection of a
CC   particular HIV strain into the transformed mammalian cell. Compounds
CC   identified can be used to treat cellular dysfunction and to prevent or
CC   combat HIV infection. The present sequence is a human chemokine receptor
CC   (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for
CC   entry mediated by the envelope glycoproteins of primary macrophage-tropic
CC   strains of HIV-1.
XX
SQ   Sequence   352 AA;

  Query Match           85.4%;  Score 958;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 15
AAB46858
ID   AAB46858 standard; Protein; 352 AA.
XX
AC   AAB46858;
XX
DT   16-AUG-2001  (updated)
DT   02-AUG-2001  (updated)
DT   04-MAY-2001  (first entry)
XX
DE   Human HDGNR10 protein.
XX
KW   HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
KW   immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
KW   cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
KW   vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
KW   angiogenesis; solid tumour; infection; leukemia; growth factor activity;
```

```
SQ   Sequence   352 AA;

  Query Match             85.4%;  Score 958;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

```
RESULT 12
AAE07048
ID   AAE07048 standard; Protein; 352 AA.
XX
AC   AAE07048;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX
KW   Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW   human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
KW   cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
KW   neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW   rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW   gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW   haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW   multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW   cardiovascular disorder; myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO200158916-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04153.
XX
PR   09-FEB-2000; 2000US-0181258.
PR   09-MAR-2000; 2000US-0187999.
PR   22-SEP-2000; 2000US-0234336.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Roschke V,  Li Y,  Ruben SM;
XX
DR   WPI; 2001-488966/53.
DR   N-PSDB; AAD13299.
XX
PT   Isolated nucleic acid encoding a human G-protein chemokine receptor
PT   (CCR5) HDGNR10 polypeptide, useful for preventing or treating
PT   autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
PT   disorders and neurodegenerative disorders -
XX
PS   Example 40; Page 504-505; 518pp; English.
XX
CC   The invention relates to human G-protein chemokine receptor (CCR5)
CC   HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies
CC   are useful for treating, preventing or ameliorating a disease or disorder
CC   associated with inflammation, defective or aberrant chemotaxis of immune
CC   cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
CC   sarcoma) or defective or aberrant T-cell antigen presenting cell
CC   interaction. The disease or disorder may also be an infectious disease
CC   (e.g. a viral infection such as an early stage HIV infection, a
CC   cytomegalovirus infection, or a poxvirus infection), an autoimmune
CC   disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
CC   disease or disorder may be associated with aberrant CCR5 expression, lack
CC   of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
CC   function. CCR5 HDGNR10 protein is used as a food additive or preservative
CC   to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
CC   for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
CC   protein, antibodies, agonists and antagonists are also useful in the
CC   diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC   gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC   urogenital); immune disorders (Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis); cardiovascular disorders (myocardial ischaemias) and
CC   wound healing. The present sequence is human CCR5 HDGNR10 protein.
XX
SQ   Sequence   352 AA;

  Query Match             85.4%;  Score 958;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

```
RESULT 13
AAB83354
ID   AAB83354 standard; Protein; 352 AA.
XX
AC   AAB83354;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human CCR5 protein sequence.
XX
KW   Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
KW   human immunodeficiency virus; anti-inflammatory disease; human.
XX
OS   Homo sapiens.
XX
PN   EP1118858-A2.
XX
PD   25-JUL-2001.
XX
PF   03-JAN-2001; 2001EP-0300020.
XX
PR   12-JAN-2000; 2000GB-0000659.
PR   12-JAN-2000; 2000GB-0000661.
PR   12-JAN-2000; 2000GB-0000663.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Dobbs S,  Perros M,  Rickett GA;
XX
```

```
KW   CCR5; chemokine; co-receptor; human immunodeficiency virus type 1;
KW   HIV-1; infection; therapy; vaccine; anti-HIV-1.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    2..18
FT                   /note= "binds to HIV-1 gp120"
XX
PN   WO200164710-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06699.
XX
PR   29-FEB-2000; 2000US-185667P.
PR   19-MAY-2000; 2000US-205839P.
PR   07-FEB-2001; 2001US-267231P.
XX
PA   (PROG-) PROGENICS PHARM INC.
PA   (AARO-) AARON DIAMOND AIDS RES CENT.
XX
PI   Dragic T,  Olson WC;
XX
DR   WPI; 2001-611273/70.
DR   N-PSDB; AAH26903.
XX
PT   Novel compounds comprising specific amino acids within CCR5 (HIV 1
PT   co-receptor) amino terminal domain including negatively charged and two
PT   sulfated tyrosine residues is useful for treating HIV infection in
PT   humans -
XX
PS   Claim 1; Page 30; 163pp; English.
XX
CC   The present sequence is that of human HIV-1 co-receptor CCR5.
CC   Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1
CC   gp120-binding site that determines the specificity of the
CC   interaction between CCR5 and HIV-1 gp120.  Post-translational
CC   sulfation of the tyrosine residues in the CCR5 N-terminus is
CC   required for gp120 binding and may critically modulate the
CC   susceptibility of target cells to HIV-1 infection in vivo.  The
CC   invention provides claimed sulfated peptides (see AAB82947) that
CC   are based on the CCR5 N-terminal region and which are effective
CC   for inhibiting HIV-1 binding to CCR5.  These peptides are used in
CC   claimed methods of inhibiting HIV infection of CD4+ cells, of
CC   preventing CD4+ cells from becoming infected with HIV, of treating
CC   a subject whose CD4+ cells are infected with HIV, and of
CC   identifying an agent which inhibits binding of a CCR5 ligand to a
CC   CCR5 receptor.  The methods may be carried out in a subject,
CC   especially a human, infected (therapeutic method), not infected
CC   with HIV (prophylactic method), or in a subject who is not infected
CC   with, but has been exposed to, HIV.
XX
SQ   Sequence   352 AA;

  Query Match             85.4%;  Score 958;  DB 22;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 11
AAE07039
ID   AAE07039 standard; Protein; 352 AA.
XX
AC   AAE07039;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX
KW   Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW   human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
KW   cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
KW   neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW   rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW   gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW   haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW   multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW   cardiovascular disorder; myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO200158915-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04152.
XX
PR   09-FEB-2000; 2000US-0181258.
PR   09-MAR-2000; 2000US-0187999.
PR   22-SEP-2000; 2000US-0234336.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Roschke V,  Li Y,  Ruben SM;
XX
DR   WPI; 2001-488965/53.
DR   N-PSDB; AAD13198.
XX
PT   Isolated nucleic acid encoding a human G-protein chemokine receptor
PT   (CCR5) HDGNR10 polypeptide, useful for preventing or treating
PT   autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
PT   disorders and neurodegenerative disorders -
XX
PS   Example 40; Page 486-487; 495pp; English.
XX
CC   The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
CC   protein. CCR5 HDGNR10 antibodies are useful for treating, preventing
CC   or ameliorating a disease or disorder associated with inflammation,
CC   defective or aberrant chemotaxis of immune cells, HIV infection (such as
CC   Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
CC   aberrant T-cell antigen presenting cell interaction. The disease or
CC   disorder may also be an infectious disease (e.g. a viral infection such
CC   as an early stage HIV infection, a cytomegalovirus infection, or a
CC   poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
CC   a neurodegenerative disorder. The disease or disorder may be associated
CC   with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
CC   ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
CC   is used as a food additive or preservative to increase or decrease
CC   storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
CC   identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
CC   antibodies, agonists and antagonists are also useful in the
CC   diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC   gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC   urogenital); immune disorders (Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis); cardiovascular disorders (myocardial ischaemias) and
CC   wound healing.
XX
```

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177172-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US11098.
XX
PR 07-APR-2000; 2000US-195747P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX
DR WPI; 2001-648759/74.
DR N-PSDB; ABI97978.
XX
PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PT versions of GPCRs -
XX
PS Claim 1; Page 277-278; 394pp; English.
XX
CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such
CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence is a non-endogenous
CC version of a known human GPCR.
XX
SQ Sequence 352 AA;

Query Match 85.4%; Score 958; DB 22; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-105;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy 181 HFPY 184
Db 181 HFPY 184

RESULT 9
AAG80111
ID AAG80111 standard; Protein; 352 AA.
XX
AC AAG80111;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CCR5 protein.
XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX

OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP03708.
XX
PR 31-MAR-2000; 2000DE-1016013.
XX
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsberg N;
XX
DR WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands,
PT useful for detecting tumors, inflammation etc., also therapeutic use of
PT ligand inhibitors -
XX
PS Disclosure; Page 10; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention.
XX
SQ Sequence 352 AA;

Query Match 85.4%; Score 958; DB 22; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-105;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy 181 HFPY 184
Db 181 HFPY 184

RESULT 10
AAB82948
ID AAB82948 standard; Protein; 352 AA.
XX
AC AAB82948;
XX
DT 21-DEC-2001 (first entry)
XX
DE Human HIV-1 co-receptor CCR5.
XX

```
CC   CC chemokine receptor that has been designated CCR5.  The sequence
CC   was deduced from an isolated cDNA clone (see AAT76920).  An Ala127Leu
CC   variant (see W238340 of CCR5 was also identified.  The susceptibility
CC   of human macrophages to HIV infection depends on cell surface
CC   expression of CD4 and CCR5.  CCR5 is a member of the 7-transmembrane
CC   superfamily of G-protein coupled cell surface molecules.  It plays
CC   an essential role in the membrane fusion step of infection by some
CC   HIV isolates.  The establishment of stable, non-human cell lines
CC   and transgenic mammals having cells that coexpress human CD4 and
CC   CCR5 provides valuable tools for research of HIV infection.
CC   Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
CC   agents capable of blocking membrane fusion between HIV and target
CC   cells represent potential anti-HIV therapeutics for macrophage
CC   tropic strains of HIV.
XX
SQ   Sequence   352 AA;

  Query Match           85.4%;  Score 958;  DB 19;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 7
AAW88232
ID   AAW88232 standard; Protein; 352 AA.
XX
AC   AAW88232;
XX
DT   15-MAR-1999  (first entry)
XX
DE   HIV-1 co-receptor CCR5.
XX
KW   HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
KW   gene therapy; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          32..56
FT                   /note= "transmembrane domain 1"
FT   Domain          67..87
FT                   /note= "transmembrane domain 2"
FT   Misc-difference 101
FT                   /note= "corresponds to TGT (Cys) in wild-type CCR5,
FT                        TGA (Stop) in CCr5m303"
FT   Domain          103..124
FT                   /note= "transmembrane domain 3"
FT   Domain          142..167
FT                   /note= "transmembrane domain 4"
FT   Domain          200..223
FT                   /note= "transmembrane domain 5"
FT   Domain          236..260
FT                   /note= "transmembrane domain 6"
FT   Domain          275..301
FT                   /note= "transmembrane domain 7"
FT
XX
PN   WO9854317-A1.
XX
PD   03-DEC-1998.
XX
PF   29-MAY-1998;   98WO-EP03437.
XX
PR   30-MAY-1997;   97US-0048057.
XX
PA   (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
PI   Arenzana Siesdedos F,  Beretta A,  Braun J,  Quillent C;
XX
DR   WPI; 1999-059835/05.
DR   N-PSDB; AAV84126.
XX
PT   New CCR5 variant protein of the HIV-1 co-receptor - useful in
PT   developing resistance of CCR5-expressing cells to HIV-1 infection
XX
PS   Disclosure; Page 34-35; 55pp; English.
XX
CC   This is the amino acid sequence of wild-type human CCR5, which
CC   serves as a co-receptor for infection by macrophage-tropic
CC   (M-tropic) strains of HIV-1.  The invention relates to the
CC   identification of a CCR5 variant (see AAW88231), designated CCR5m303,
CC   comprising the first two transmembrane domains of wild-type CCR5,
CC   but lacking transmembrane domains 3-7.  The presence of the
CC   CCR5m303 variant with the wild type CCR5 allele shows a positive
CC   correlation with resistance to infection with M-tropic HIV-1
CC   strains, and may indicate slower progression of the disease.  The
CC   detection of CCR5 variants may be used to identify individuals at
CC   lower risk of infection relative to the general population who, if
CC   infected, may exhibit slower progression to AIDS.  Probes and
CC   primers (see AAV84127-36) are provided for use in diagnostic methods
CC   for detecting the presence of such variants.  A method is provided
CC   for inhibiting HIV-1 infection of a cell expressing the CCR5
CC   receptor.  This involves introducing a nucleic acid encoding a CCR5
CC   variant into the cell, thereby reducing the number of functional
CC   CCR5 molecules present on the cell surface.
XX
SQ   Sequence   352 AA;

  Query Match           85.4%;  Score 958;  DB 20;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1e-105;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 8
ABB56342
ID   ABB56342 standard; Protein; 352 AA.
XX
AC   ABB56342;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Non-endogenous human GPCR protein, SEQ ID NO: 477.
XX
KW   Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW   constitutively activated GPCR; agonist; disease.
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:16:36 ; Search time 19.7178 Seconds
(without alignments)
1048.235 Million cell updates/sec

Title: US-09-939-226-6
Perfect score: 1122
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASVSK 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	958	85.4	352	2	A43113	chemokine (C-C) re
2	694	61.9	360	2	JC2443	chemokine (C-C) re
3	694	61.9	374	2	I38450	chemokine (C-C) re
4	598	53.3	355	2	A45177	chemokine (C-C) re
5	573.5	51.1	355	2	I49339	macrophage inflamm
6	547.5	48.8	360	2	A57160	chemokine (C-C) re
7	546.5	48.7	360	2	JC4587	chemokine (C-C) re
8	535.5	47.7	359	2	I49341	MIP-1 alpha recept
9	506.5	45.1	355	2	G02436	chemokine (C-C) re
10	489.5	43.6	356	2	I49340	MIP-1 alpha recept
11	449	40.0	383	2	S55594	G protein-coupled
12	427.5	38.1	355	2	JC5067	G protein-coupled
13	386	34.4	354	2	I58186	probable G protein
14	378	33.7	344	2	JC5942	chemokine receptor
15	365	32.5	355	2	JC4304	orphan G protein-c
16	345.5	30.8	378	2	B55735	lymphocyte-specifi
17	342.5	30.5	378	2	A55735	G protein-coupled
18	333.5	29.7	378	2	A45680	G protein-coupled
19	331.5	29.5	352	2	A45747	neuropeptide Y/pep
20	326	29.1	353	2	S28787	neuropeptide Y/pep
21	325.5	29.0	352	2	G00048	fusin (LESTRA) - c
22	321.5	28.7	359	2	I51372	angiotensin II rec
23	320	28.5	369	2	JC5068	G protein-coupled
24	317	28.3	359	2	JC1194	angiotensin II rec
25	314	28.0	359	2	A42656	angiotensin II rec
26	312	27.8	359	2	JC1104	angiotensin II rec
27	312	27.8	359	2	I39418	angiotensin II rec
28	311	27.7	359	2	JC2134	angiotensin II rec
29	310	27.6	359	2	S15403	angiotensin II rec
30	309	27.5	359	2	JH0621	angiotensin II rec
31	308	27.5	359	2	A48857	angiotensin II rec
32	307	27.4	359	2	S44425	angiotensin II rec
33	306	27.3	359	2	JQ1516	angiotensin II rec
34	291	25.9	350	2	JN0621	G protein-coupled
35	287.5	25.6	367	2	JE0349	interferon-inducib
36	283	25.2	362	2	JN0694	angiotensin II rec
37	276	24.6	333	2	I65989	G protein-coupled
38	276	24.6	363	2	I57955	somatostatin recep
39	276	24.6	364	2	JN0763	somatostatin recep
40	274.5	24.5	359	2	A48921	interleukin-8 rece
41	273.5	24.4	384	2	A47249	brain-specific som
42	270.5	24.1	388	2	JN0605	somatostatin recep
43	269	24.0	360	2	A53611	interleukin-8 rece
44	267	23.8	363	2	I57940	somatostatin recep
45	265	23.6	355	2	JQ1231	interleukin-8 rece

ALIGNMENTS

RESULT 1
A43113
chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine rece
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarag
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184,'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a d
nd may have had a selective advantage by conferring resistance to Yersinia plague inf
R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine
A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemok
A;Reference number: A58833; MUID:96291862; PMID:8663314

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A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTE
A;Note: probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F;32-56/Domain: transmembrane #status predicted <TM1>
F;67-87/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;142-166/Domain: transmembrane #status predicted <TM4>
F;193-218/Domain: transmembrane #status predicted <TM5>
F;236-257/Domain: transmembrane #status predicted <TM6>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

  Query Match            85.4%;  Score 958;  DB 2;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-80;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmemb
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

  Query Match            61.9%;  Score 694;  DB 2;  Length 360;
  Best Local Similarity  75.9%;  Pred. No. 2.4e-56;
  Matches  132;  Conservative   17;  Mismatches   23;  Indels    2;  Gaps    1;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
              :|||||||||||||||||||:||||||:||||||: |||   | |  :||
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195


RESULT 3
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte c
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38450
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmemb
F;44-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM6>
F;292-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;32-277,113-190/Disulfide bonds: #status predicted

  Query Match            61.9%;  Score 694;  DB 2;  Length 374;
  Best Local Similarity  75.9%;  Pred. No. 2.5e-56;
  Matches  132;  Conservative   17;  Mismatches   23;  Indels    2;  Gaps    1;

Qy         10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
              :| :|    || | :|||| |:||||||||||||||||||||:|||||||:|| :|||||
Db         24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

Qy         70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
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```
                ||||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||||
Db         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
              :|||||||||||||||||||||||:||||||:||||||: |||   | |  :||
Db        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195


RESULT 4
A45177
chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-
A;Reference number: A45177; MUID:93161416; PMID:7679328
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alph
A;Reference number: I55671; MUID:93240122; PMID:7683036
A;Accession: I55671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

  Query Match             53.3%;  Score 598;  DB 2;  Length 355;
  Best Local Similarity   59.2%;  Pred. No. 1.6e-47;
  Matches  109;  Conservative   34;  Mismatches   37;  Indels    4;  Gaps    2;

Qy          2 DYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL 61
              ||  ::   : :|  : ||||:| :   |:||||||||||: | |||:||:|:|:  |||
Db          9 DYDTTT---EFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYKRL 65

Qy         62 KSMTDIYLLNLAISDLFFLLTVPFWAHYAAA-QWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |:|| |||||||||| || |:|||  |     | ||: ||:|:|: |: | :| |||||
Db         66 KNMTSIYLLNLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFFII 125

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||:||||||||:||:| | :|: ||:||: |:::| |  |:|||
Db        126 LLTIDRYLAIVHAVFALRARTVTFGVITSIIIWALAILASMPGLYFSKTQWEFTHHTCSL 185

Qy        181 HFPY 184
              ||||:
Db        186 HFPH 189
```

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RESULT 5
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chem
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <RES>
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin

  Query Match             51.1%;  Score 573.5;  DB 2;  Length 355;
  Best Local Similarity   61.1%;  Pred. No. 2.9e-45;
  Matches  107;  Conservative   27;  Mismatches   40;  Indels    1;  Gaps    1;

Qy         11 DINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLL 70
              : :|  | ||||  |:   | ||||||||||| | |||:||||:|:  :||:||| |||
Db         15 EFDYGDSTPCQKTAVRAFGAGLLPPLYSLVFIIGVVGNVLVILVLMQHRRLQSMTSIYLF 74

Qy         71 NLAISDLFFLLTVPFWAHYAAA-QWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
              |||:||| || |:|||  |     | ||: ||:||:| |::| :| |||||||||||||
Db         75 NLAVSDLVFLFTLPFWIDYKLKDDWIFGDAMCKLLSGFYYLGLYSEIFFIILLTIDRYLA 134

Qy        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPY 184
              :|||||||:||||| |::||:||| :|: ||:| : | ::| |  | ||| ||||
Db        135 IVHAVFALRARTVTLGIITSIITWALAILASMPALYFFKAQWEFTHRTCSPHFPY 189


RESULT 6
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicto

  Query Match             48.8%;  Score 547.5;  DB 2;  Length 360;
  Best Local Similarity   54.1%;  Pred. No. 7.1e-43;
  Matches  100;  Conservative   36;  Mismatches   44;  Indels    5;  Gaps    2;
```

```
Qy          2 DYQVSSPIYDINYYTSE----PCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILIN 57
              |  :   ||  |||  |    || |  :|      |||||||||:|| :|| :|:|:|
Db          8 DTTLDESIYS-NYYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFK 66

Qy         58 CKRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIF 117
               |||:||||:|||||||||| |: ::||| :||| || ||  :|:::: :| :|||:||||
Db         67 YKRLRSMTDVYLLNLAISDLLFVFSLPFWGYYAADQWVFGLGLCKMISWMYLVGFYSGIF 126

Qy        118 FIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYT 177
              |::|::|||||:|||||:|:|||:|:||:||: || |||||||| :|:    |  |
Db        127 FVMLMSIDRYLAIVHAVFSLRARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTY 186

Qy        178 CSSHF 182
              |:: :
Db        187 CKTKY 191


RESULT 7
JC4587
chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match             48.7%;  Score 546.5;  DB 2;  Length 360;
  Best Local Similarity   55.9%;  Pred. No. 8.8e-43;
  Matches   99;  Conservative   36;  Mismatches   39;  Indels    3;  Gaps    1;

Qy          9 IYDINYY---TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMT 65
              :|:  |:     :|| |  :|      |||||||||: |  || :|:|:|   |||||||
Db         15 VYNSYYFYESMPKPCTKEGIKAFGEVFLPPLYSLVFLLGLFGNSVVVLVLFKYKRLKSMT 74

Qy         66 DIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTID 125
              |:|||||||||| |:|::||| :||| || ||  :|:::: :| :||:|||||||:|::||
Db         75 DVYLLNLAISDLLFVLSLPFWGYYAADQWVFGLGLCKIVSWMYLVGFYSGIFFIMLMSID 134

Qy        126 RYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHF 182
              ||||:|||||:|||||:|:||:||:||:||| |||||||||::|:    |  |  | : :
Db        135 RYLAIVHAVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTCYTEHNHTYCKTQY 191


RESULT 8
I49341
MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C;Accession: I49341
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

  Query Match             47.7%;  Score 535.5;  DB 2;  Length 359;
  Best Local Similarity   57.9%;  Pred. No. 9e-42;
  Matches   99;  Conservative   31;  Mismatches   40;  Indels    1;  Gaps    1;

Qy         14 YYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLA 73
              |  : ||:|: :|:: : |||||||||| | :|||:|:|||| ::|: ||:||| |||
Db         22 YEWAPPCEKVRIKELGSWLLPPLYSLVFIIGLLGNMMVVLILIKYRKLQIMTNIYLFNLA 81

Qy         74 ISDLFFLLTVPFWAHYAA-AQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVH 132
              |||| || ||||| ||    :| ||: ||::|:| |::  :| ||||||||||||||:||
Db         82 ISDLLFLFTVPFWIHYVLWNEWGFGHYMCKMLSGFYYLALYSEIFFIILLTIDRYLAIVH 141

Qy        133 AVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
              |||||:||||||  :||:||| :|  |:||  ||  ||     ::||  :|
Db        142 AVFALRARTVTFATITSIITWGLAGLAALPEFIFHESQDSFGEFSCSPRYP 192


RESULT 9
G02436
chemokine (C-C) receptor 3 - human
N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accession: G02436; A57237
R;Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A;Reference number: H01272
A;Accession: G02436
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <PON>
A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561
R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine recepto
A;Reference number: A57237; MUID:95348056; PMID:7622448
A;Accession: A57237
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504
C;Genetics:
A;Gene: GDB:CMKBR3
A;Cross-references: GDB:579624; OMIM:601268
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte

  Query Match             45.1%;  Score 506.5;  DB 2;  Length 355;
  Best Local Similarity   57.6%;  Pred. No. 4.2e-39;
  Matches   95;  Conservative   32;  Mismatches   37;  Indels    1;  Gaps    1;

Qy         20 CQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFF 79
              |:| : : : |: :|||||||  | :||::|::|||  :||: ||:|||||||||| |
Db         24 CEKADTRALMAQFVPPLYSLVFTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLF 83

Qy         80 LLTVPFWAHYAAA-QWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALK 138
              |:|:||| ||     | ||: ||:||:| |  | :| ||||||||||||||:|||||||:
Db         84 LVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143
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Qy        139 ARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
              ||||||||:||::|| :|| |:||  ||  :::      ||: :|
Db        144 ARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYP 188


RESULT 10
I49340
MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-356 <RES>
A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin

  Query Match             43.6%;  Score 489.5;  DB 2;  Length 356;
  Best Local Similarity   51.1%;  Pred. No. 1.5e-37;
  Matches   94;  Conservative   34;  Mismatches   51;  Indels    5;  Gaps    2;

Qy          5 VSSPIYDI----NYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |: | |:     :: :   |  |||:     :  |||||||| | :|::||:|:||  ||
Db          6 VTEPSYNTVAKNDFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKR 65

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHY-AAAQWDFGNTMCQLLTGLYFIGFFSGIFFI 119
              |::|| ||| ||||||| || |:|||   |      | ||| ||: ::| |::| :| :|||
Db         66 LRNMTSIYLFNLAISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYYLGLYSDMFFI 125

Qy        120 ILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCS 179
              |||||||||||| |||||:|||||||:::|:|||||:|   |:| :   :|| |  ::||
Db        126 TLLTIDRYLAVVHVVFALRARTVTFGIISSIITWVLAALVSIPCLYVFKSQMEFTYHTCR 185

Qy        180 SHFP 183
              :  |
Db        186 AILP 189


RESULT 11
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S55594
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-383 <TEL>
A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match             40.0%;  Score 449;  DB 2;  Length 383;
  Best Local Similarity   48.6%;  Pred. No. 8.7e-34;
  Matches   85;  Conservative   37;  Mismatches   51;  Indels    2;  Gaps    1;

Qy         11 DINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLL 70
              |::|  | || | :  ::||:::| || |||:|| :||:||::|:|   ::|::|:: ||
Db         53 DVDYEESAPCYKSDTTRLAAQVVPALYLLVFLFGLLGNILVVIIVIRYMKIKNLTNMLLL 112

Qy         71 NLAISDLFFLLTVPFWAHYAAA--QWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYL 128
              ||||||| ||||:||| ||      | || ::|:|| |: ::  :| :| |||||:||||
Db        113 NLAISDLLFLLTLPFWMHYIGMYHDWTFGISLCKLLRGVCYMSLYSQVFCIILLTVDRYL 172

Qy        129 AVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
              |||:|| ||: |||| |:|| | || :|   |||   |   | :     |  ::|
Db        173 AVVYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFHGHQDDNGRVQCDPYYP 227


RESULT 12
JC5067
G protein-coupled receptor CKR-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Accession: JC5067; G02776; G02387
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5067
A;Molecule type: DNA
A;Residues: 1-355 <ZAB>
A;Cross-references: EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01714
A;Accession: G02776
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R;Bonner, T.I.
submitted to the EMBL Data Library, January 1996
A;Reference number: H01154
A;Accession: G02387
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <BON>
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
A;Cross-references: GDB:6053733; OMIM:601834
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;36-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;200-222/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM6>
F;281-304/Domain: transmembrane #status predicted <TM7>

  Query Match             38.1%;  Score 427.5;  DB 2;  Length 355;
  Best Local Similarity   42.8%;  Pred. No. 7.6e-32;
  Matches   80;  Conservative   40;  Mismatches   62;  Indels    5;  Gaps    2;

Qy          1 MDYQVSSPIYDI-NYY----TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILIL 55
              ||| :   :  : :||     | ||    ::     ||   | |:|:|  :|| ||||:|
Db          1 MDYTLDLSVTTVTDYYYPDIFSSPCDAELIQTNGKLLLAVFYCLLFVFSLLGNSLVILVL 60

Qy         56 INCKRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSG 115
              : ||:|:|:||:||||||:||| |: : ||  :|   || ||  ||::::| |:|||:|
Db         61 VVCKKLRSITDVYLLNLALSDLLFVFSFPFQTYYLLDQWVFGTVMCKVVSGFYYIGFYSS 120

Qy        116 IFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLH 175
              :||| |:::|||||||||||:||| ||:  |    :  |: |: |::| ::| :   |
Db        121 MFFITLMSVDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGV 180

Qy        176 YTCSSHF 182
                | | :
Db        181 LQCYSFY 187


RESULT 13
```

```
I58186
probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: I58186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b
A;Reference number: I58186; MUID:94323113; PMID:8047298
A;Accession: I58186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match             34.4%;  Score 386;  DB 2;  Length 354;
  Best Local Similarity   42.4%;  Pred. No. 5e-28;
  Matches   78;  Conservative   31;  Mismatches   67;  Indels    8;  Gaps    2;

Qy          6 SSPIYDINYY----TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL 61
              | |  |:  :    ::| |   ::        |   ||||| || |||:||:| | | ::
Db          4 SFPELDLENFEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTFGLVGNLLVVLALTNSRKS 63

Qy         62 KSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIIL 121
              ||:||||||||:||| |: |:||| ||  :     | ||:| |  :|||| |||| : .
Db         64 KSITDIYLLNLALSDLLFVATLPFWTHYLISHEGLHNAMCKLTTAFFFIGFFGGIFFITV 123

Qy        122 LTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSH 181
              ::|||||:| |  ::  |||  ||  |:  |  |:  : |  :||: :       |
Db        124 ISIDRYLAIVLAANSMNNRTVQHGVTISLGVWAAAILVASPQFMFTKRKDN----ECLGD 179

Qy        182 FPYI 185
              :| :
Db        180 YPEV 183


RESULT 14
JC5942
chemokine receptor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5942
R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor.
A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <FAN>
A;Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
C;Superfamily: vertebrate rhodopsin

  Query Match             33.7%;  Score 378;  DB 2;  Length 344;
  Best Local Similarity   44.4%;  Pred. No. 2.6e-27;
  Matches   76;  Conservative   34;  Mismatches   53;  Indels    8;  Gaps    3;

Qy         17 SEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISD 76
              :| | | : : ::|:|:| | | ||: | : |:||:|||:  | || : :|||||||:|:
Db         25 AEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAVSN 84

Qy         77 LFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVH-AVF 135
              | ||||:|||||        |: ||::| ||||:| :|  ||  |||: |||  :|   |
Db         85 LCFLLTLPFWAHAG------GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKGNF 138

Qy        136 ALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCS-SHFPYI 185
                 | |  |::|||: || |: |:||  :  : | |   | |: |  |::
Db        139 FSARRRVPCGIITSVLAWVTAILATLPEYVVYKPQMEDQKYKCAFSRTPFL 189


RESULT 15
```

```
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related t
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular sig
C;Comment: This protein is a key regulator of many immune and homeostatic responses,
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

  Query Match             32.5%;  Score 365;  DB 2;  Length 355;
  Best Local Similarity   43.2%;  Pred. No. 4.3e-26;
  Matches   73;  Conservative   28;  Mismatches   64;  Indels    4;  Gaps    2;

Qy         17 SEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISD 76
              :| |   ::       |   ||::|  | |||:||:  | | |: ||:|||||||||:||
Db         18 AEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSD 77

Qy         77 LFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFA 136
              | |: |:||| ||   :    | ||:  |  :|||||  |||| :::|||||:| |  :
Db         78 LLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANS 137

Qy        137 LKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYI 185
              :  |||  ||  |:  |  |:  : |  :||: |||     |  :| :
Db        138 MNNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKEN---ECLGDYPEV 182


Search completed: June  3, 2003, 15:22:40
Job time : 19.7178 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:09:40 ; Search time 9.85891 Seconds
(without alignments)
904.503 Million cell updates/sec

Title: US-09-939-226-6
Perfect score: 1122
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASVSK 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	958	85.4	352	1	CKR5_HUMAN	P51681 homo sapien
2	952	84.8	352	1	CKR5_PANTR	P56440 pan troglod
3	947	84.4	352	1	CKR5_PONPY	O97881 pongo pygma
4	942	84.0	352	1	CKR5_GORGO	P56439 gorilla gor
5	938	83.6	352	1	CKR5_PYGBI	O97880 pygathrix b
6	938	83.6	352	1	CKR5_PYGNE	O97882 pygathrix n
7	938	83.6	352	1	CKR5_TRAFR	O97878 trachypithe
8	938	83.6	352	1	CKR5_TRAPH	O97879 trachypithe
9	936	83.4	352	1	CKR5_HYLLE	O97883 hylobates l
10	933	83.2	352	1	CKR5_MACMU	P79436 macaca mula
11	933	83.2	352	1	CKR5_PAPHA	P56441 papio hamad
12	928	82.7	352	1	CKR5_CERTO	O62743 cercocebus
13	916	81.6	352	1	CKR5_CERAE	P56493 cercopithec
14	786	70.1	354	1	CKR5_MOUSE	P51682 mus musculu
15	775	69.1	354	1	CKR5_RAT	O08556 rattus norv
16	715.5	63.8	373	1	CKR2_MOUSE	P51683 mus musculu
17	714.5	63.7	373	1	CKR2_RAT	O55193 rattus norv
18	694	61.9	374	1	CKR2_HUMAN	P41597 homo sapien
19	688	61.3	360	1	CKR2_MACMU	O18793 macaca mula
20	598	53.3	355	1	CKR1_HUMAN	P32246 homo sapien
21	570.5	50.8	355	1	CKR1_MOUSE	P51675 mus musculu
22	562	50.1	355	1	CKR1_MACMU	P56482 macaca mula
23	547.5	48.8	360	1	CKR4_HUMAN	P51679 homo sapien
24	546.5	48.7	360	1	CKR4_MOUSE	P51680 mus musculu
25	535.5	47.7	359	1	CKR3_MOUSE	P51678 mus musculu
26	535.5	47.7	359	1	CKR3_RAT	O54814 rattus norv
27	516.5	46.0	358	1	CKR3_CAVPO	Q9z213 cavia porce
28	506.5	45.1	355	1	CKR3_HUMAN	P51677 homo sapien
29	499.5	44.5	355	1	CKR3_MACMU	P56483 macaca mula
30	489.5	43.6	355	1	CKR3_CERAE	P56492 cercopithec
31	489.5	43.6	356	1	CKRV_MOUSE	P51676 mus musculu
32	431	38.4	353	1	CKR8_MOUSE	P56484 mus musculu
33	427.5	38.1	355	1	CKR8_HUMAN	P51685 homo sapien
34	424	37.8	356	1	CKR8_MACMU	O97665 macaca mula
35	386	34.4	354	1	C3X1_RAT	P35411 rattus norv
36	383	34.1	354	1	C3X1_MOUSE	Q9z0d9 mus musculu
37	370	33.0	369	1	CKR9_MOUSE	Q9wut7 mus musculu
38	365	32.5	355	1	C3X1_HUMAN	P49238 homo sapien
39	363	32.4	357	1	CKR9_HUMAN	P51686 homo sapien
40	345.5	30.8	378	1	CKR7_HUMAN	P32248 homo sapien
41	342.5	30.5	378	1	CKR7_MOUSE	P47774 mus musculu
42	334.5	29.8	352	1	CCR4_CERTO	O62747 cercocebus
43	331.5	29.5	352	1	CCR4_HUMAN	P30991 homo sapien
44	331.5	29.5	352	1	CCR4_MACMU	P79394 macaca mula
45	330.5	29.5	384	1	CKD6_HUMAN	O00590 homo sapien

ALIGNMENTS

RESULT 1
CKR5_HUMAN
ID CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; Q9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CCR5 OR CMKBR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
RT CC-chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RT RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N.; Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).

```
RN   [6]
RP   SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX   MEDLINE=98022612; PubMed=9359654;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98049523; PubMed=9388201;
RA   Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT   "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT   with 5'-end heterogeneity, dual promoter usage, and evidence for
RT   polymorphisms within the regulatory regions and noncoding exons.";
RL   J. Biol. Chem. 272:30662-30671(1997).
RN   [8]
RP   SEQUENCE FROM N.A., AND VARIANT ARG-178.
RA   Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
RA   Debre P.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX   MEDLINE=96260017; PubMed=8649511;
RA   Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
RA   di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
RA   Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT   "Identification of a major co-receptor for primary isolates of
RT   HIV-1.";
RL   Nature 381:661-666(1996).
RN   [10]
RP   CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX   MEDLINE=96260018; PubMed=8649512;
RA   Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RA   Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
RA   Paxton W.A.;
RT   "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
RT   CC-CKR-5.";
RL   Nature 381:667-673(1996).
RN   [11]
RP   SULFATION.
RX   MEDLINE=99189752; PubMed=10089882;
RA   Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA   Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT   "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT   entry.";
RL   Cell 96:667-676(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC       SYNCYTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC       VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC   -!- PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
CC   -!- PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
CC       GLYCOSYLATION.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X91492; CAA62796.1; -.
DR   EMBL; U54994; AAC50598.1; -.
DR   EMBL; U57840; AAB17071.1; -.
DR   EMBL; U95626; AAB57793.1; -.
DR   EMBL; U83326; AAC51797.1; -.
DR   EMBL; AF011500; AAB65700.1; -.
DR   EMBL; AF011501; AAB65701.1; -.
DR   EMBL; AF011502; AAB65702.1; -.
DR   EMBL; AF011503; AAB65703.1; -.
DR   EMBL; AF011505; AAB65705.1; -.
DR   EMBL; AF011506; AAB65706.1; -.
DR   EMBL; AF011507; AAB65707.1; -.
DR   EMBL; AF011508; AAB65708.1; -.
DR   EMBL; AF011509; AAB65709.1; -.
DR   EMBL; AF011510; AAB65710.1; -.
DR   EMBL; AF011511; AAB65711.1; -.
DR   EMBL; AF011512; AAB65712.1; -.
DR   EMBL; AF011513; AAB65713.1; -.
DR   EMBL; AF011514; AAB65714.1; -.
DR   EMBL; AF011515; AAB65715.1; -.
DR   EMBL; AF011516; AAB65716.1; -.
DR   EMBL; AF011517; AAB65717.1; -.
DR   EMBL; AF011518; AAB65718.1; -.
DR   EMBL; AF011519; AAB65719.1; -.
DR   EMBL; AF011520; AAB65720.1; -.
DR   EMBL; AF011521; AAB65721.1; -.
DR   EMBL; AF011522; AAB65722.1; -.
DR   EMBL; AF011523; AAB65723.1; -.
DR   EMBL; AF011524; AAB65724.1; -.
DR   EMBL; AF011525; AAB65725.1; -.
DR   EMBL; AF011526; AAB65726.1; -.
DR   EMBL; AF011527; AAB65727.1; -.
DR   EMBL; AF011528; AAB65728.1; -.
DR   EMBL; AF011529; AAB65729.1; -.
DR   EMBL; AF011530; AAB65730.1; -.
DR   EMBL; AF011531; AAB65731.1; -.
DR   EMBL; AF011532; AAB65732.1; -.
DR   EMBL; AF011533; AAB65733.1; -.
DR   EMBL; AF011534; AAB65734.1; -.
DR   EMBL; AF011535; AAB65735.1; -.
DR   EMBL; AF011536; AAB65736.1; -.
DR   EMBL; AF011537; AAB65737.1; -.
DR   EMBL; AF031237; AAB94735.1; -.
DR   EMBL; AF052539; AAD18131.1; -.
DR   Genew; HGNC:1606; CCR5.
DR   MIM; 601373; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW   Polymorphism.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      31    58       1 (POTENTIAL).
FT   DOMAIN        59    68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      69    89       2 (POTENTIAL).
FT   DOMAIN        90    102      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      103   124      3 (POTENTIAL).
FT   DOMAIN        125   141      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      142   166      4 (POTENTIAL).
FT   DOMAIN        167   198      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      199   218      5 (POTENTIAL).
FT   DOMAIN        219   235      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      236   260      6 (POTENTIAL).
FT   DOMAIN        261   277      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      278   301      7 (POTENTIAL).
FT   DOMAIN        302   352      CYTOPLASMIC (POTENTIAL).
FT   DISULFID      101   178      BY SIMILARITY.
FT   MOD_RES       3     3        SULFATION.
FT   MOD_RES       10    10       SULFATION.
FT   MOD_RES       14    14       SULFATION.
FT   MOD_RES       15    15       SULFATION.
FT   VARIANT       10    10       Y -> D (IN INCCR5-71A).
FT                                /FTId=VAR_003481.
FT   VARIANT       29    29       A -> S (IN DBSNP:1800939).
FT                                /FTId=VAR_011839.
FT   VARIANT       31    31       R -> H (IN INCCR5-72A).
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  Query Match             85.4%;  Score 958;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-53;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 2
CKR5_PANTR
ID   CKR5_PANTR     STANDARD;      PRT;   352 AA.
AC   P56440; O02778;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98022612; PubMed=9359654;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97426118; PubMed=9282822;
RA   Zacharova V., Zachar V., Goustin A.S.;
RT   "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT   HIV type 1 host.";
RL   AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98090115; PubMed=9430250;
RA   Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT   "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL   AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF005663; AAB62557.1; -.
DR   EMBL; U94329; AAB58446.1; -.
DR   EMBL; AF011542; AAB65742.1; -.
DR   EMBL; U97666; AAC51670.1; -.
DR   EMBL; AF011540; AAB65740.1; -.
DR   EMBL; U89797; AAC03717.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
FT   CARBOHYD    268    268       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    123    123       T -> S (IN REF. 1).
SQ   SEQUENCE   352 AA;  40539 MW;  4A33E698B80FE34C CRC64;

  Query Match             84.8%;  Score 952;  DB 1;  Length 352;
  Best Local Similarity   98.9%;  Pred. No. 5.4e-53;
  Matches  182;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 3
CKR5_PONPY
ID   CKR5_PONPY     STANDARD;      PRT;   352 AA.
AC   O97881;
DT   30-MAY-2000 (Rel. 39, Created)
```

```
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075446; AAD19858.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40527 MW;  F4E2F47135AF658A CRC64;

  Query Match             84.4%;  Score 947;  DB 1;  Length 352;
  Best Local Similarity   98.4%;  Pred. No. 1.1e-52;
  Matches  181;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 4
CKR5_GORGO
ID   CKR5_GORGO     STANDARD;      PRT;   352 AA.
AC   P56439;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF005659; AAB62553.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40515 MW;  D0E6FCB9FE5EAC84 CRC64;
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  Query Match             84.0%;  Score 942;  DB 1;  Length 352;
  Best Local Similarity   97.8%;  Pred. No. 2.3e-52;
  Matches  180;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKTNVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 5
CKR5_PYGBI
ID   CKR5_PYGBI     STANDARD;      PRT;   352 AA.
AC   O97880;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=61621;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075445; AAD19857.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40585 MW;  4366F142730F938F CRC64;

  Query Match             83.6%;  Score 938;  DB 1;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 4e-52;
  Matches  177;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 6
CKR5_PYGNE
ID   CKR5_PYGNE     STANDARD;      PRT;   352 AA.
AC   O97882;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Pygathrix nemaeus (Dove langur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=54133;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075448; AAD19860.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
```

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DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN       1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    31     58       1 (POTENTIAL).
FT   DOMAIN      59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    69     89       2 (POTENTIAL).
FT   DOMAIN      90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   103    124       3 (POTENTIAL).
FT   DOMAIN     125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   142    166       4 (POTENTIAL).
FT   DOMAIN     167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   199    218       5 (POTENTIAL).
FT   DOMAIN     219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   236    260       6 (POTENTIAL).
FT   DOMAIN     261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   278    301       7 (POTENTIAL).
FT   DOMAIN     302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   101    178       BY SIMILARITY.
FT   MOD_RES      3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES     10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES     14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES     15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40532 MW;  FE4F9D98D3B3E861 CRC64;

  Query Match             83.6%;  Score 938;  DB 1;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 4e-52;
  Matches  177;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 7
CKR5_TRAFR
ID   CKR5_TRAFR     STANDARD;      PRT;   352 AA.
AC   O97878;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Trachypithecus.
OX   NCBI_TaxID=54180;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075442; AAD19854.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN       1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    31     58       1 (POTENTIAL).
FT   DOMAIN      59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    69     89       2 (POTENTIAL).
FT   DOMAIN      90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   103    124       3 (POTENTIAL).
FT   DOMAIN     125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   142    166       4 (POTENTIAL).
FT   DOMAIN     167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   199    218       5 (POTENTIAL).
FT   DOMAIN     219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   236    260       6 (POTENTIAL).
FT   DOMAIN     261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   278    301       7 (POTENTIAL).
FT   DOMAIN     302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   101    178       BY SIMILARITY.
FT   MOD_RES      3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES     10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES     14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES     15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40496 MW;  4366F148C255938F CRC64;

  Query Match             83.6%;  Score 938;  DB 1;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 4e-52;
  Matches  177;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 8
CKR5_TRAPH
ID   CKR5_TRAPH     STANDARD;      PRT;   352 AA.
AC   O97879;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Trachypithecus phayrei (Phayre's leaf monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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OC   Trachypithecus.
OX   NCBI_TaxID=61618;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075443; AAD19855.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40509 MW;  4366F148D3A5938F CRC64;

  Query Match            83.6%;  Score 938;  DB 1;  Length 352;
  Best Local Similarity  96.2%;  Pred. No. 4e-52;
  Matches  177;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
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RESULT 9
CKR5_HYLLE
ID   CKR5_HYLLE     STANDARD;      PRT;   352 AA.
AC   O97883;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Hylobates leucogenys (White-cheeked gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=61853;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075451; AAD19863.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
SQ   SEQUENCE   352 AA;  40445 MW;  4F8E4F344CEB7C91 CRC64;

  Query Match            83.4%;  Score 936;  DB 1;  Length 352;
  Best Local Similarity  97.3%;  Pred. No. 5.4e-52;
  Matches  179;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:| ||||||||||||||||||||||||||||||||:||||||
Db          1 MDYQVSSPTYDIDYDTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILVLINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 10
CKR5_MACMU
ID   CKR5_MACMU     STANDARD;      PRT;   352 AA.
AC   P79436; O02746;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Macaca mulatta (Rhesus macaque),
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544, 9541, 9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta;
RX   MEDLINE=97184592; PubMed=9032394;
RA   Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA   Newman W., Gerard N., Gerard C., Sodroski J.;
RT   "Utilization of C-C chemokine receptor 5 by the envelope
RT   glycoproteins of a pathogenic simian immunodeficiency virus,
RT   SIVmac239.";
RL   J. Virol. 71:2522-2527(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta; STRAIN=Indian macaque;
RX   MEDLINE=97213934; PubMed=9060623;
RA   Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT   "Genetically divergent strains of simian immunodeficiency virus use
RT   CCR5 as a coreceptor for entry.";
RL   J. Virol. 71:2705-2714(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta;
RX   MEDLINE=21354176; PubMed=11461684;
RA   Margulies B.J., Hauer D.A., Clements J.E.;
RT   "Identification and comparison of eleven rhesus macaque chemokine
RT   receptors.";
RL   AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U77672; AAC51109.1; -.
DR   EMBL; U73739; AAC51158.1; -.
DR   EMBL; U96762; AAC34132.1; -.
DR   EMBL; AF005660; AAB62554.1; -.
DR   EMBL; AF005661; AAB62555.1; -.
DR   EMBL; AF005662; AAB62556.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN       1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    31     58       1 (POTENTIAL).
FT   DOMAIN      59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    69     89       2 (POTENTIAL).
FT   DOMAIN      90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   103    124       3 (POTENTIAL).
FT   DOMAIN     125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   142    166       4 (POTENTIAL).
FT   DOMAIN     167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   199    218       5 (POTENTIAL).
FT   DOMAIN     219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   236    260       6 (POTENTIAL).
FT   DOMAIN     261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   278    301       7 (POTENTIAL).
FT   DOMAIN     302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   101    178       BY SIMILARITY.
FT   MOD_RES      3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES     10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES     14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES     15     15       SULFATION (BY SIMILARITY).
FT   CARBOHYD   268    268       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   241    241       M -> I (IN REF. 3).
FT   CONFLICT   292    292       I -> M (IN REF. 3).
SQ   SEQUENCE   352 AA;  40507 MW;  58B96C85909FACB2 CRC64;

  Query Match           83.2%;  Score 933;  DB 1;  Length 352;
  Best Local Similarity 96.2%;  Pred. No. 8.3e-52;
  Matches  177;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 11
CKR5_PAPHA
ID   CKR5_PAPHA     STANDARD;      PRT;   352 AA.
AC   P56441;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
```

```
GN   CCR5 OR CMKBR5.
OS   Papio hamadryas (Hamadryas baboon), and
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9557, 9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=P.hamadryas;
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=P.hamadryas;
RX   MEDLINE=99210133; PubMed=10195758;
RA   Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT   "Species-specific changes in the CCR5 gene from African and Asian
RT   nonhuman primates.";
RL   AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=P.anubis;
RA   Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF005658; AAB62552.1; -.
DR   EMBL; AF105287; AAD20556.1; -.
DR   EMBL; AF105288; AAD20557.1; -.
DR   EMBL; AF105289; AAD20558.1; -.
DR   EMBL; AF105290; AAD20559.1; -.
DR   EMBL; AF023452; AAC63830.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
FT   CARBOHYD    268    268       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   352 AA;  40489 MW;  5E1504A9BA1FE8B2 CRC64;

  Query Match             83.2%;  Score 933;  DB 1;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 8.3e-52;
  Matches  177;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||:
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 12
CKR5_CERTO
ID   CKR5_CERTO     STANDARD;      PRT;   352 AA.
AC   O62743; O62744; O62745; O62746;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Isolate 079, 085, 087, and 089;
RX   MEDLINE=98321155; PubMed=9656999;
RA   Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT   "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT   naturally infected in west Africa: a comparison of coreceptor usage
RT   of primary SIVsm, HIV-2, and SIVmac.";
RL   Virology 246:113-124(1998).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF051902; AAC39830.1; -.
DR   EMBL; AF051903; AAC39831.1; -.
DR   EMBL; AF051904; AAC39832.1; -.
DR   EMBL; AF051905; AAC39833.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
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DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      14     14       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
FT   VARIANT       2      2       D -> E (IN ISOLATE 087).
FT   VARIANT       3      3       Y -> D (IN ISOLATE 079).
FT   VARIANT      25     25       V -> G (IN ISOLATE 087).
FT   VARIANT     100    100       M -> K (IN ISOLATE 079).
FT   VARIANT     107    107       L -> V (IN ISOLATE 089).
FT   VARIANT     134    134       V -> G (IN ISOLATE 079).
FT   VARIANT     146    146       V -> L (IN ISOLATES 085 AND 089).
FT   VARIANT     340    340       T -> I (IN ISOLATE 079).
SQ   SEQUENCE   352 AA;  40489 MW;  20A196E2D47E49CA CRC64;

  Query Match             82.7%;  Score 928;  DB 1;  Length 352;
  Best Local Similarity   95.7%;  Pred. No. 1.7e-51;
  Matches  176;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSP 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 13
CKR5_CERAE
ID   CKR5_CERAE     STANDARD;      PRT;   352 AA.
AC   P56493;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=98001387; PubMed=9343222;
RA   Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT   "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT   implicate specific amino acids in infections by simian and human
RT   immunodeficiency viruses.";
RL   J. Virol. 71:8642-8656(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT   "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT   gene.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC       DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U83324; AAC51795.1; -.
DR   EMBL; U83325; AAC51796.1; -.
DR   EMBL; AB015944; BAA31328.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW   Polymorphism.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       2 (POTENTIAL).
FT   DOMAIN       90    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    124       3 (POTENTIAL).
FT   DOMAIN      125    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    260       6 (POTENTIAL).
FT   DOMAIN      261    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    301       7 (POTENTIAL).
FT   DOMAIN      302    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    101    178       BY SIMILARITY.
FT   MOD_RES       3      3       SULFATION (BY SIMILARITY).
FT   MOD_RES      10     10       SULFATION (BY SIMILARITY).
FT   MOD_RES      15     15       SULFATION (BY SIMILARITY).
FT   VARIANT      14     14       N -> Y.
FT   VARIANT     352    352       F -> L.
SQ   SEQUENCE   352 AA;  40561 MW;  7F52E690C72EC29A CRC64;

  Query Match             81.6%;  Score 916;  DB 1;  Length 352;
  Best Local Similarity   95.1%;  Pred. No. 9.4e-51;
  Matches  175;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||: ||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||| |||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPRIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 14
CKR5_MOUSE
ID   CKR5_MOUSE     STANDARD;      PRT;   354 AA.
AC   P51682; Q61867; P97405; O35313; P97308; O35891;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE   alpha receptor).
GN   CCR5 OR CMKBR5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Spleen;
RX   MEDLINE=96205938; PubMed=8631787;
RA   Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA   Charo I.F.;
RT   "Molecular cloning and functional expression of murine JE (monocyte
RT   chemoattractant protein 1) and murine macrophage inflammatory protein
RT   1alpha receptors: evidence for two closely linked C-C chemokine
RT   receptors on chromosome 9.";
RL   J. Biol. Chem. 271:7551-7558(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX   MEDLINE=96278910; PubMed=8662890;
RA   Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT   "Cloning and characterization of a novel murine macrophage
RT   inflammatory protein-1 alpha receptor.";
RL   J. Biol. Chem. 271:14445-14451(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Ola;
RA   Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6, and NIH Swiss; TISSUE=Liver, Kidney, and Spleen;
RX   MEDLINE=98001387; PubMed=9343222;
RA   Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT   "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT   implicate specific amino acids in infections by simian and human
RT   immunodeficiency viruses.";
RL   J. Virol. 71:8642-8656(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=97404635; PubMed=9261347;
RA   Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA   Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT   "Two distinct CCR5 domains can mediate coreceptor usage by human
RT   immunodeficiency virus type 1.";
RL   J. Virol. 71:6305-6314(1997).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Guo B., Kuno K., Harada A., Matsushima K.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
CC       BUT NOT IN NONHEMATOPOIETIC CELL LINES.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U47036; AAC52454.1; -.
DR   EMBL; X94151; CAA63867.1; -.
DR   EMBL; U68565; AAB37273.1; -.
DR   EMBL; U83327; AAC53386.1; -.
DR   EMBL; AF022990; AAC53389.1; -.
DR   EMBL; AF019772; AAB71183.1; -.
DR   EMBL; D83648; BAA12024.1; -.
DR   MGD; MGI:107182; Cmkbr5.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     33     60       1 (POTENTIAL).
FT   DOMAIN       61     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     91       2 (POTENTIAL).
FT   DOMAIN       92    104       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    105    126       3 (POTENTIAL).
FT   DOMAIN      127    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    168       4 (POTENTIAL).
FT   DOMAIN      169    200       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    201    220       5 (POTENTIAL).
FT   DOMAIN      221    237       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    238    262       6 (POTENTIAL).
FT   DOMAIN      263    279       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    280    303       7 (POTENTIAL).
FT   DOMAIN      304    354       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    103    180       BY SIMILARITY.
FT   CARBOHYD    270    270       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      11     11       I -> S.
FT   VARIANT      62     62       K -> R.
FT   VARIANT      66     66       V -> M.
FT   VARIANT      97     97       I -> V.
FT   VARIANT     109    109       V -> L.
FT   VARIANT     156    156       V -> A.
FT   VARIANT     160    160       F -> S.
FT   VARIANT     185    185       P -> L.
FT   VARIANT     213    213       I -> V.
FT   VARIANT     318    318       I -> M.
FT   VARIANT     337    337       V -> A.
FT   CONFLICT      3      3       F -> L (IN REF. 2).
FT   CONFLICT     80     80       L -> F (IN REF. 2).
FT   CONFLICT    145    145       N -> I (IN REF. 5).
FT   CONFLICT    190    190       H -> Y (IN REF. 3).
FT   CONFLICT    208    208       P -> S (IN REF. 1).
SQ   SEQUENCE   354 AA;  40863 MW;  B4A6B942E88F9CF0 CRC64;

  Query Match             70.1%;  Score 786;  DB 1;  Length 354;
  Best Local Similarity   80.1%;  Pred. No. 1.1e-42;
  Matches  149;  Conservative   17;  Mismatches   18;  Indels    2;  Gaps    1;

Qy          1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC 58
              ||:| | |  ||||:|  | ||||||||||||:|||||||||||||||||:| ||||:|
Db          1 MDFQGSVPTYIYIDIDYGMSAPCQKINVKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISC 60

Qy         59 KRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF 118
              |:|||:|||||||||||| ||||:|||||||| :| ||| ||:: ||:| ||:| ||||
Db         61 KKLKSVTDIYLLNLAISDLLFLLTLPFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFF 120
```

```
Qy        119 IILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTC 178
              ||||||||||:||||||| ||| |||:|||:|||||||||| |||||||||| ||||
Db        121 IILLTIDRYLAIVHAVFALKVRTVNFGVITSVVTWVVAVFASLPEIIFTRSQKEGFHYTC 180

Qy        179 SSHFPY 184
              | |||:
Db        181 SPHFPH 186


RESULT 15
CKR5_RAT
ID   CKR5_RAT       STANDARD;      PRT;   354 AA.
AC   O08556;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE   alpha receptor).
GN   CCR5 OR CMKBR5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=98334064; PubMed=9670989;
RA   Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA   Berger M., Gebicke-Haerter P.J.;
RT   "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
RT   upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL   J. Neurosci. Res. 53:16-28(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=98318173; PubMed=9655467;
RA   Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA   Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT   "Chemokine receptor expression in cultured glia and rat experimental
RT   allergic encephalomyelitis.";
RL   J. Neuroimmunol. 86:1-12(1998).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y12009; CAA72737.1; -.
DR   EMBL; U77350; AAC03243.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN       1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     33    60       1 (POTENTIAL).
FT   DOMAIN       61    70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71    91       2 (POTENTIAL).
FT   DOMAIN       92    104      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     105   126      3 (POTENTIAL).
FT   DOMAIN       127   143      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     144   168      4 (POTENTIAL).
FT   DOMAIN       169   200      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     201   220      5 (POTENTIAL).
FT   DOMAIN       221   237      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     238   262      6 (POTENTIAL).
FT   DOMAIN       263   279      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     280   303      7 (POTENTIAL).
FT   DOMAIN       304   354      CYTOPLASMIC (POTENTIAL).
FT   DISULFID     103   180      BY SIMILARITY.
FT   CARBOHYD     270   270      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   354 AA;  41030 MW;  77EDB368AA4C868D CRC64;

  Query Match             69.1%;  Score 775;  DB 1;  Length 354;
  Best Local Similarity   78.2%;  Pred. No. 5.5e-42;
  Matches  147;  Conservative   18;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC 58
              ||:| | |  ||||:|  | ||||:|||||||:||||||||||||||||||:| ||||:|
Db          1 MDFQGSIPTYIYDIDYSMSAPCQKVNVKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISC 60

Qy         59 KRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF 118
              |:|||||||| ||||||| ||||:|||||||| :| ||| ||:| ||:| ||:| ||||
Db         61 KKLKSMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGIYHIGYFGGIFF 120

Qy        119 IILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTC 178
              |||||||||||:||||||:||||| |||:|||:||||||| ||| ||| |||||| ||||
Db        121 IILLTIDRYLAIVHAVFAIKARTVNFGVITSVVTWVVAVFVSLPEIIFMRSQKEGSHYTC 180

Qy        179 SSHFPYIK 186
              | || :|:
Db        181 SPHFLHIQ 188


Search completed: June  3, 2003, 15:19:39
Job time : 10.8589 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:14:58 ; Search time 45.1235 Seconds
(without alignments)
981.754 Million cell updates/sec

Title: US-09-939-226-6
Perfect score: 1122
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASVSK 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1122	100.0	215	4	O75303	O75303 homo sapien
2	947	84.4	352	6	Q95NC5	Q95nc5 hylobates s
3	945	84.2	352	6	O18772	O18772 pan troglod
4	940	83.8	352	6	O18771	O18771 pan troglod
5	940	83.8	352	6	Q95NC0	Q95nc0 hylobates m
6	939	83.7	352	6	Q9XS99	Q9xs99 gorilla gor
7	938	83.6	352	6	Q9TV50	Q9tv50 pan troglod
8	938	83.6	352	6	Q95NC8	Q95nc8 colobus pol
9	938	83.6	352	6	Q95NC6	Q95nc6 trachypithe
10	935	83.3	352	6	Q9MZA3	Q9mza3 hylobates a
11	935	83.3	352	6	O97962	O97962 pygathrix a
12	934	83.2	352	6	Q9XT14	Q9xt14 colobus gue
13	934	83.2	352	6	Q95NC7	Q95nc7 nasalis lar
14	934	83.2	352	6	Q95NC3	Q95nc3 miopithecus
15	933	83.2	352	6	O18770	O18770 pan troglod
16	933	83.2	352	6	Q9TV49	Q9tv49 cercocebus
17	933	83.2	352	6	O97975	O97975 macaca arct
18	930	82.9	352	6	Q9TQX0	Q9tqx0 cercopithec
19	929	82.8	352	6	Q9XT12	Q9xt12 cercopithec
20	929	82.8	352	6	Q95NC1	Q95nc1 theropithec
21	927	82.6	352	6	Q9TV46	Q9tv46 cercopithec
22	927	82.6	352	6	O77776	O77776 cercocebus
23	927	82.6	352	6	Q95ND2	Q95nd2 mandrillus
24	926	82.5	352	6	Q9XT13	Q9xt13 papio anubi
25	925	82.4	352	6	Q9TSK1	Q9tsk1 cercopithec
26	925	82.4	352	6	Q9MZA2	Q9mza2 cercopithec
27	925	82.4	352	6	Q95NE8	Q95ne8 cercopithec
28	925	82.4	352	6	Q95NE1	Q95ne1 cercocebus
29	923	82.3	339	4	Q9UN28	Q9un28 homo sapien
30	923	82.3	339	4	Q9UN23	Q9un23 homo sapien
31	923	82.3	339	4	Q9UBT9	Q9ubt9 homo sapien
32	923	82.3	339	4	Q9UBJ7	Q9ubj7 homo sapien
33	922	82.2	352	6	Q9TV93	Q9tv93 macaca arct
34	922	82.2	352	6	Q95ND1	Q95nd1 mandrillus
35	922	82.2	352	6	Q95ND0	Q95nd0 erythrocebu
36	920	82.0	339	4	Q9UN27	Q9un27 homo sapien
37	920	82.0	352	6	Q9TV42	Q9tv42 cercopithec
38	919	81.9	352	6	Q9TV43	Q9tv43 cercopithec
39	919	81.9	352	6	Q9XS35	Q9xs35 macaca neme
40	917	81.7	339	6	Q9TUW7	Q9tuw7 pan troglod
41	917	81.7	339	6	Q9TUW6	Q9tuw6 pan troglod
42	917	81.7	339	6	Q9TQW4	Q9tqw4 pan troglod
43	916	81.6	352	6	Q9TV44	Q9tv44 cercopithec
44	916	81.6	352	6	Q9XT76	Q9xt76 cercopithec
45	915	81.6	352	6	Q9TV45	Q9tv45 cercopithec

ALIGNMENTS

RESULT 1
O75303
ID O75303 PRELIMINARY; PRT; 215 AA.
AC O75303;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CC-chemokine receptor.
GN CCR-5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tse L., Ehrenberg P.K., Chang G., Michael N.L.;
RT "Genomic Organization and Functional Characterization of the Complete
RT Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-
RT Receptor for HIV-1.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF009962; AAC23944.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;

Query Match 100.0%; Score 1122; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 5.8e-97;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
```

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Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215


RESULT 2
Q95NC5
ID   Q95NC5      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9590;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177884; AAK43367.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40508 MW;  F4F64B3AD5AF658A CRC64;

  Query Match             84.4%;  Score 947;  DB 6;  Length 352;
  Best Local Similarity   98.4%;  Pred. No. 1.9e-80;
  Matches  181;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 3
O18772
ID   O18772      PRELIMINARY;      PRT;   352 AA.
AC   O18772;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CCR5 receptor (Fragment).
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CHCCR5-142A;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR   EMBL; AF011541; AAB65741.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     352    352
SQ   SEQUENCE   352 AA;  40598 MW;  39688FA7004C952F CRC64;

  Query Match             84.2%;  Score 945;  DB 6;  Length 352;
  Best Local Similarity   98.4%;  Pred. No. 2.9e-80;
  Matches  181;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||||||:|||||||||||||||||||||||||||||||| ||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVDNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 4
O18771
ID   O18771      PRELIMINARY;      PRT;   352 AA.
AC   O18771;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CCR5 receptor (Fragment).
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CHCCR5-141A;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR   EMBL; AF011539; AAB65739.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     352    352
SQ   SEQUENCE   352 AA;  40466 MW;  3FFFAC7ABAE1D4FB CRC64;

  Query Match             83.8%;  Score 940;  DB 6;  Length 352;
  Best Local Similarity   97.8%;  Pred. No. 8.6e-80;
  Matches  180;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Qy          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
               |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db          61 LKSMTDIYLLNLAISNLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy         121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
               |||||||||:||||||||||||||||||||||||||||||||||||||||| ||||||||
Db         121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKGGLHYTCSS 180

Qy         181 HFPY 184
               ||||
Db         181 HFPY 184


RESULT 5
Q95NC0
ID   Q95NC0      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Hylobates moloch (silvery gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=81572;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177899; AAK43382.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40436 MW;  9623CA98340CF274 CRC64;

  Query Match             83.8%;  Score 940;  DB 6;  Length 352;
  Best Local Similarity   97.8%;  Pred. No. 8.6e-80;
  Matches  180;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
               |||||||| |||:|||| ||||||||||||||||||||||||||||||||||||||||||
Db           1 MDYQVSSPTYDIDYYTSGPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy         121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
               |||||||||:||||||||||||||||||||||||||||||||||||||||| ||||||||
Db         121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKGGLHYTCSS 180

Qy         181 HFPY 184
               ||||
Db         181 HFPY 184


RESULT 6
Q9XS99
ID   Q9XS99      PRELIMINARY;      PRT;   352 AA.
AC   Q9XS99;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CC chemokine receptor 5.
GN   CCR5.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GORILLACCR;
RX   MEDLINE=99210133; PubMed=10195758;
RA   Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;
RT   "Species-specific changes in the CCR5 gene from African and Asian
RT   nonhuman primates.";
RL   AIDS Res. Hum. Retroviruses 15:479-483(1999).
DR   EMBL; AF105291; AAD20560.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40529 MW;  1BE68C68FE2E7AD0 CRC64;

  Query Match             83.7%;  Score 939;  DB 6;  Length 352;
  Best Local Similarity   97.3%;  Pred. No. 1.1e-79;
  Matches  179;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
               |||||||| |||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db           1 MDYQVSSPTYDIDYYTSEPCQKTNVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy         121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
               |||||||||:||||||||||||||||:||||||||||||||||||||||||||||||||
Db         121 LLTIDRYLAIVHAVFALKARTVTFGLVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy         181 HFPY 184
               ||||
Db         181 HFPY 184


RESULT 7
Q9TV50
ID   Q9TV50      PRELIMINARY;      PRT;   352 AA.
AC   Q9TV50;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CC chemokine receptor type 5.
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1410;
RX   MEDLINE=99335215; PubMed=10408730;
RA   Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA   Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT   "Mutations in CCR5-coding sequences are not associated with SIV
RT   carrier status in African nonhuman primates.";
RL   AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1410;
RA   Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA   Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF035214; AAD44007.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
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DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40481 MW;  2578A0F2C07A4A65 CRC64;

  Query Match           83.6%;  Score 938;  DB 6;  Length 352;
  Best Local Similarity   96.7%;  Pred. No. 1.3e-79;
  Matches  178;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||||||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||:||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 8
Q95NC8
ID   Q95NC8      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Colobus polykomos.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Colobus.
OX   NCBI_TaxID=9572;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177881; AAK43364.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40578 MW;  4366F149C3B4938F CRC64;

  Query Match           83.6%;  Score 938;  DB 6;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 1.3e-79;
  Matches  177;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 9
Q95NC6
ID   Q95NC6      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Trachypithecus johnii (hooded leaf monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Trachypithecus.
OX   NCBI_TaxID=66063;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177883; AAK43366.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40462 MW;  52824E0322559F7F CRC64;

  Query Match           83.6%;  Score 938;  DB 6;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 1.3e-79;
  Matches  177;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 10
Q9MZA3
ID   Q9MZA3      PRELIMINARY;      PRT;   352 AA.
AC   Q9MZA3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CC chemokine receptor 5.
GN   CCR5.
OS   Hylobates agilis unko.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9583;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20317091; PubMed=10747879;
RA   Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
RA   Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K.,
RA   Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
RT   "Evolution of human and non-human primate CC chemokine receptor 5 gene
RT   and mRNA. Potential roles for haplotype and mRNA diversity,
RT   differential haplotype-specific transcriptional activity, and altered
RT   transcription factor binding to polymorphic nucleotides in the
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RT   pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL   J. Biol. Chem. 275:18946-18961(2000).
DR   EMBL; AF252551; AAF87981.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40293 MW;  BAF8279ABBAB5309 CRC64;

  Query Match             83.3%;  Score 935;  DB 6;  Length 352;
  Best Local Similarity   96.7%;  Pred. No. 2.5e-79;
  Matches  178;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPTYDIDYYTSGPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDVYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTATFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 11
O97962
ID   O97962      PRELIMINARY;    PRT;   352 AA.
AC   O97962;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   C-C chemokine receptor type 5.
GN   CCR5.
OS   Pygathrix avunculus (Tonkin snub-nosed monkey), and
OS   Pygathrix roxellana (golden snub-nosed monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=66062, 61622;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y.-W., Zhang Y.-P.;
RT   "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF075447; AAD19859.1; -.
DR   EMBL; AF075444; AAD19856.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40482 MW;  037CFA9E12E532F3 CRC64;

  Query Match             83.3%;  Score 935;  DB 6;  Length 352;
  Best Local Similarity   95.7%;  Pred. No. 2.5e-79;
  Matches  176;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:|||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTATFGVVTSVITWVVAVFASLPGIIFTRSQREGVHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 12
Q9XT14
ID   Q9XT14      PRELIMINARY;      PRT;   352 AA.
AC   Q9XT14;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CC chemokine receptor 5.
GN   CCR5.
OS   Colobus guereza (Black-and-white colobus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Colobus.
OX   NCBI_TaxID=33548;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spearman P.W., Mburu D.N., Graham B.S.;
RT   "Differential Utilization of CCR5 Molecules from Three East African
RT   Simian Species by the HIV-1 Envelope Glycoprotein.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF141639; AAD32684.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40550 MW;  9B078EF04D34DB36 CRC64;

  Query Match             83.2%;  Score 934;  DB 6;  Length 352;
  Best Local Similarity   95.7%;  Pred. No. 3.1e-79;
  Matches  176;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAIVHAVFALKARTATFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 13
Q95NC7
ID   Q95NC7      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Nasalis larvatus (Proboscis monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Nasalis.
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OX   NCBI_TaxID=43780;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177882; AAK43365.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40537 MW;  51F6F1486E35938E CRC64;

  Query Match             83.2%;  Score 934;  DB 6;  Length 352;
  Best Local Similarity   95.7%;  Pred. No. 3.1e-79;
  Matches  176;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAARWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 14
Q95NC3
ID   Q95NC3      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Miopithecus.
OX   NCBI_TaxID=36231;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177886; AAK43369.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40546 MW;  6464152F3E566AE5 CRC64;

  Query Match             83.2%;  Score 934;  DB 6;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 3.1e-79;
  Matches  177;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCRLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 15
O18770
ID   O18770      PRELIMINARY;      PRT;   352 AA.
AC   O18770;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CCR5 receptor (Fragment).
GN   CCR5.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MACCR5-140A;
RA   Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA   Ho D.D.;
RT   "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL   AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR   EMBL; AF011538; AAB65738.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     352     352
SQ   SEQUENCE   352 AA;  40523 MW;  4513DB983A28ACB2 CRC64;

  Query Match             83.2%;  Score 933;  DB 6;  Length 352;
  Best Local Similarity   96.2%;  Pred. No. 3.8e-79;
  Matches  177;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              |||||||| |||:|||||||||:|||||||||||||||||||||||:||:||||||||
Db          1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              |||||||||:|||||||||||||||||||||||||||||||||||||||||:||||||||
Db        121 LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


Search completed: June  3, 2003, 15:21:41
Job time : 45.1235 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:19:46 ; Search time 78.2222 Seconds
(without alignments)
947.732 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1005926 seqs, 210607049 residues

Total number of hits satisfying chosen parameters: 1005926

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	100.0	352	1	PCT-US02-29560-259	Sequence 259, App
2	1841	100.0	352	1	PCT-US02-06345-1	Sequence 1, Appli
3	1841	100.0	352	1	PCT-US03-03763-1	Sequence 1, Appli
4	1841	100.0	352	5	US-09-949-002-303	Sequence 303, App
5	1841	100.0	352	5	US-09-949-004-242	Sequence 242, App
6	1841	100.0	352	6	US-10-086-814-1	Sequence 1, Appli
7	1841	100.0	352	6	US-10-245-882-259	Sequence 259, App
8	1841	100.0	352	6	US-10-323-314-1	Sequence 1, Appli
9	1841	100.0	352	6	US-10-225-567A-352	Sequence 352, App
10	1841	100.0	352	6	US-10-290-058A-6	Sequence 6, Appli
11	1841	100.0	352	6	US-10-360-828-1	Sequence 1, Appli
12	1841	100.0	352	6	US-10-239-423-67	Sequence 67, Appl
13	1841	100.0	352	7	US-60-452-680-12568	Sequence 12568, A
14	1841	100.0	352	7	US-60-453-135-7850	Sequence 7850, Ap
15	1841	100.0	352	7	US-60-453-050-7850	Sequence 7850, Ap
16	1841	100.0	352	7	US-60-455-444-4380	Sequence 4380, Ap
17	1841	100.0	352	7	US-60-465-241-4380	Sequence 4380, Ap
18	1841	100.0	352	7	US-60-466-412-7850	Sequence 7850, Ap
19	1841	100.0	378	5	US-09-949-002-552	Sequence 552, App
20	1841	100.0	378	5	US-09-949-004-442	Sequence 442, App
21	1641.5	89.2	332	6	US-10-095-876A-2	Sequence 2, Appli
22	1547	84.0	354	6	US-10-219-051B-10290	Sequence 10290, A
23	1547	84.0	354	6	US-10-219-051B-10294	Sequence 10294, A
24	1364	74.1	360	6	US-10-225-567A-460	Sequence 460, App
25	1364	74.1	360	6	US-10-239-423-64	Sequence 64, Appl
26	1364	74.1	360	7	US-60-452-680-12372	Sequence 12372, A
27	1364	74.1	360	7	US-60-453-135-7700	Sequence 7700, Ap
28	1364	74.1	360	7	US-60-453-050-7700	Sequence 7700, Ap
29	1364	74.1	360	7	US-60-455-444-4289	Sequence 4289, Ap
30	1364	74.1	360	7	US-60-465-241-4289	Sequence 4289, Ap
31	1364	74.1	360	7	US-60-466-412-7700	Sequence 7700, Ap
32	1364	74.1	377	5	US-09-949-004-443	Sequence 443, App
33	1364	74.1	377	5	US-09-949-016-11221	Sequence 11221, A
34	1339	72.7	268	6	US-10-160-619-164	Sequence 164, App
35	1335	72.5	268	6	US-10-160-619-162	Sequence 162, App
36	1283.5	69.7	384	5	US-09-893-512A-14	Sequence 14, Appl
37	1224	66.5	374	5	US-09-949-004-244	Sequence 244, App
38	1224	66.5	374	5	US-09-893-512A-13	Sequence 13, Appl
39	1224	66.5	374	6	US-10-239-423-63	Sequence 63, Appl
40	1224	66.5	374	6	US-10-219-051B-10292	Sequence 10292, A
41	1224	66.5	374	6	US-10-219-051B-10296	Sequence 10296, A
42	1224	66.5	374	7	US-60-452-680-12373	Sequence 12373, A
43	1224	66.5	374	7	US-60-453-135-7701	Sequence 7701, Ap
44	1224	66.5	374	7	US-60-453-050-7701	Sequence 7701, Ap
45	1224	66.5	374	7	US-60-455-444-4290	Sequence 4290, Ap

ALIGNMENTS

RESULT 1
PCT-US02-29560-259
; Sequence 259, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; CURRENT FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 259
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560-259

Query Match 100.0%; Score 1841; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 2
PCT-US02-06345-1
; Sequence 1, Application PC/TUS0206345
; GENERAL INFORMATION:
;  APPLICANT: Progenics Pharmaceuticals, Inc., et al.
;  TITLE OF INVENTION: Sulfated CCR5 Peptides For HIV-1 Infection
;  FILE REFERENCE: 61010-AB1-PCT/JPW/JTL
;  CURRENT APPLICATION NUMBER: PCT/US02/06345
;  CURRENT FILING DATE: 2002-02-28
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
PCT-US02-06345-1

  Query Match            100.0%;  Score 1841;  DB 1;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 3
PCT-US03-03763-1
; Sequence 1, Application PC/TUS0303763
; GENERAL INFORMATION:
;  APPLICANT: Hua, Shaobing
;  APPLICANT:  Pauling, Michelle H.
;  APPLICANT:  Zhu, Li
;  TITLE OF INVENTION: METHODS FOR GENERATING ANTIBODIES AGAINST MEMBRANE PROTEINS
;  FILE REFERENCE: 25636-728
;  CURRENT APPLICATION NUMBER: PCT/US03/03763
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 10/071,866
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 10/072,301
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 10/133,978
;  PRIOR FILING DATE: 2002-04-25
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US03-03763-1

  Query Match            100.0%;  Score 1841;  DB 1;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 4
US-09-949-002-303
; Sequence 303, Application US/09949002
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 303
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-002-303

  Query Match            100.0%;  Score 1841;  DB 5;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 5
US-09-949-004-242
; Sequence 242, Application US/09949004
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000848
;  CURRENT APPLICATION NUMBER: US/09/949,004
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: 60/232,045
;  PRIOR FILING DATE: 2000-09-13
;  NUMBER OF SEQ ID NOS: 6961
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 242
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-004-242

  Query Match             100.0%;  Score 1841;  DB 5;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 6
US-10-086-814-1
; Sequence 1, Application US/10086814
; GENERAL INFORMATION:
;  APPLICANT: Dragic, Tatjana
;  APPLICANT:  Olson, William C.
;  TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE: 61010-AB-1
;  CURRENT APPLICATION NUMBER: US/10/086,814
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-086-814-1

  Query Match             100.0%;  Score 1841;  DB 6;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 7
US-10-245-882-259
; Sequence 259, Application US/10245882
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Wilson, Keith E.
;  APPLICANT:  Zlotnik, Albert
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-002710US
;  CURRENT APPLICATION NUMBER: US/10/245,882
;  CURRENT FILING DATE:  2002-12-13
;  PRIOR APPLICATION NUMBER: US 60/323,469
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/323,887
;  PRIOR FILING DATE: 2001-09-20
;  PRIOR APPLICATION NUMBER: US 60/325,114
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/340,944
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/355,145
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/355,257
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/369,899
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 412
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 259
```

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;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-245-882-259

  Query Match            100.0%;  Score 1841;  DB 6;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 8
US-10-323-314-1
; Sequence 1, Application US/10323314
; GENERAL INFORMATION:
;  APPLICANT: Dragic, Tatjana
;  APPLICANT:  Olson, William
;  TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
;  CURRENT APPLICATION NUMBER: US/10/323,314
;  CURRENT FILING DATE:  2002-12-19
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: human
US-10-323-314-1

  Query Match            100.0%;  Score 1841;  DB 6;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 9
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-567A-352

  Query Match            100.0%;  Score 1841;  DB 6;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 10
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; GENERAL INFORMATION:
;  APPLICANT: Silos-Santiago, Inmaculada
;  TITLE OF INVENTION: Methods and Compositions for Treating
;  TITLE OF INVENTION:  Urological Disorders Using 313, 333, 5464, 18817 or 33524
;  FILE REFERENCE: MPI01-289P1RM
;  CURRENT APPLICATION NUMBER: US/10/290,058A
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: 60/344,552
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 6
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-290-058A-6

  Query Match             100.0%;  Score 1841;  DB 6;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 11
US-10-360-828-1
; Sequence 1, Application US/10360828
; GENERAL INFORMATION:
;  APPLICANT: Hua, Shaobing
;  APPLICANT:  Pauling, Michelle H.
;  APPLICANT:  Zhu, Li
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
;  FILE REFERENCE: 25636-727
;  CURRENT APPLICATION NUMBER: US/10/360,828
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 10/071,866
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 10/072,301
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 10/133,978
;  PRIOR FILING DATE: 2002-04-25
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-360-828-1

  Query Match             100.0%;  Score 1841;  DB 6;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 12
US-10-239-423-67
; Sequence 67, Application US/10239423
; GENERAL INFORMATION:
;  APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
;  APPLICANT:  HEITLAND, Aleksandra; SPODSBERG, Nikolaj
;  TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
;  TITLE OF INVENTION:  Cell Surface Proteome of Tumor and Inflammation Cells and
;  TITLE OF INVENTION:  for Treating Tumor Diseases and Inflammatory Diseases,
;  TITLE OF INVENTION:  Preferably with the Aid of Specific Chemokine
;  TITLE OF INVENTION:  Receptor Analysis and Chemokine Receptor/Ligand Interaction
;  FILE REFERENCE: 022217us
;  CURRENT APPLICATION NUMBER: US/10/239,423
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: DE10016013.1
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67

  Query Match             100.0%;  Score 1841;  DB 6;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 13
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US-60-452-680-12568
; Sequence 12568, Application US/60452680
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  GRUPE, Andrew
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001450
;  CURRENT APPLICATION NUMBER: US/60/452,680
;  CURRENT FILING DATE:  2003-03-07
;  NUMBER OF SEQ ID NOS: 116213
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12568
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-452-680-12568

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  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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Db        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352


RESULT 14
US-60-453-135-7850
; Sequence 7850, Application US/60453135
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001456
;  CURRENT APPLICATION NUMBER: US/60/453,135
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7850
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-135-7850

  Query Match           100.0%;  Score 1841;  DB 7;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300

Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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US-60-453-050-7850
; Sequence 7850, Application US/60453050
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  LUKE, May
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001457
;  CURRENT APPLICATION NUMBER: US/60/453,050
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7850
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-050-7850

  Query Match           100.0%;  Score 1841;  DB 7;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-171;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Qy        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240

Qy        241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Job time : 80.2222 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:19:11 ; Search time 170.635 Seconds
(without alignments)
812.364 Million cell updates/sec

Title: US-09-939-226-6
Perfect score: 1122
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASVSK 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1122	100.0	215	20	US-09-626-939-6	Sequence 6, Appli
3	1122	100.0	215	23	US-09-938-703-6	Sequence 6, Appli
4	1122	100.0	215	23	US-09-938-719-6	Sequence 6, Appli
5	1122	100.0	215	23	US-09-939-226-6	Sequence 6, Appli
6	969.5	86.4	191	27	US-60-182-562-1416	Sequence 1416, Ap
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8	958	85.4	184	20	US-09-626-939-4	Sequence 4, Appli
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15	958	85.4	352	1	PCT-US01-10708-3	Sequence 3, Appli
16	958	85.4	352	1	PCT-US02-03634-22	Sequence 22, Appl
17	958	85.4	352	10	US-08-661-393-2	Sequence 2, Appli
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20	958	85.4	352	15	US-09-195-662A-2	Sequence 2, Appli
21	958	85.4	352	17	US-09-339-912A-2	Sequence 2, Appli
22	958	85.4	352	19	US-09-502-783A-2	Sequence 2, Appli
23	958	85.4	352	19	US-09-502-784A-2	Sequence 2, Appli
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26	958	85.4	352	21	US-09-725-285-2	Sequence 2, Appli
27	958	85.4	352	21	US-09-734-221A-14	Sequence 14, Appl
28	958	85.4	352	21	US-09-759-841-2	Sequence 2, Appli
29	958	85.4	352	21	US-09-779-879A-22	Sequence 22, Appl
30	958	85.4	352	21	US-09-779-880A-22	Sequence 22, Appl
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32	958	85.4	352	22	US-09-813-653-15	Sequence 15, Appl
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35	958	85.4	352	23	US-09-938-719-5	Sequence 5, Appli
36	958	85.4	352	23	US-09-939-226-5	Sequence 5, Appli
37	958	85.4	352	24	US-10-067-800-22	Sequence 22, Appl
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39	958	85.4	352	24	US-10-072-301-1	Sequence 1, Appli
40	958	85.4	352	25	US-10-106-623-2	Sequence 2, Appli
41	958	85.4	352	25	US-10-133-978-1	Sequence 1, Appli
42	958	85.4	352	25	US-10-135-839-22	Sequence 22, Appl
43	958	85.4	352	26	US-10-232-686-2	Sequence 2, Appli
44	953	84.9	309	27	US-60-229-515-844	Sequence 844, App
45	953	84.9	352	12	US-08-864-458-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-626-500-6
; Sequence 6, Application US/09626500
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/626,500
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,752

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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  215 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-626-500-6

  Query Match           100.0%;  Score 1122;  DB 20;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-103;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215


RESULT 2
US-09-626-939-6
; Sequence 6, Application US/09626939
;  GENERAL INFORMATION:
;    APPLICANT:  SAMSON, MICHEL
;    APPLICANT:  PARMENTIER, MARC
;    APPLICANT:  VASSART, GILBERT
;    APPLICANT:  LIBERT, FREDERICK
;    TITLE OF INVENTION:  ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;    TITLE OF INVENTION:  AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/626,939
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/833,752
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  215 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-626-939-6

  Query Match           100.0%;  Score 1122;  DB 20;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-103;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215


RESULT 3
US-09-938-703-6
; Sequence 6, Application US/09938703
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/938,703
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 2000-07-27
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;    INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 215 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

  Query Match           100.0%;  Score 1122;  DB 23;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-103;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215


RESULT 4
US-09-938-719-6
; Sequence 6, Application US/09938719
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/938,719
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 27-JULY-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 215 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

  Query Match           100.0%;  Score 1122;  DB 23;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-103;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215


RESULT 5
US-09-939-226-6
; Sequence 6, Application US/09939226
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/939,226
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 2000-07-27
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 215 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6

  Query Match           100.0%;  Score 1122;  DB 23;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-103;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
              |||||||||||||||||||||||||||||||||||
Db        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215


RESULT 6
US-60-182-562-1416
; Sequence 1416, Application US/60182562
```

```
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION: PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL000247
;  CURRENT APPLICATION NUMBER: US/60/182,562
;  CURRENT FILING DATE: 2000-02-15
;  NUMBER OF SEQ ID NOS: 1658
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1416
;   LENGTH: 191
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-182-562-1416

  Query Match             86.4%;  Score 969.5;  DB 27;  Length 191;
  Best Local Similarity   99.0%;  Pred. No. 2.4e-88;
  Matches  189;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         26 KQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFFLLTVPF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFFLLTVPF 60

Qy         86 WAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALKARTVTFG 145
              |||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 WAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVFHAVFALKARTVTFG 120

Qy        146 VVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPY-IKDSHLGAGPAAACHGHLLL 204
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        121 VVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYNIKDSHLGAGPAAACHGHLLL 180

Qy        205 GNPKNSASVSK 215
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Db        181 GNPKNSASVSK 191


RESULT 7
US-09-626-500-4
; Sequence 4, Application US/09626500
;  GENERAL INFORMATION:
;    APPLICANT:  SAMSON, MICHEL
;    APPLICANT:  PARMENTIER, MARC
;    APPLICANT:  VASSART, GILBERT
;    APPLICANT:  LIBERT, FREDERICK
;    TITLE OF INVENTION:  ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;    TITLE OF INVENTION:  AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/626,500
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/833,752
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  184 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-626-500-4

  Query Match             85.4%;  Score 958;  DB 20;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 8
US-09-626-939-4
; Sequence 4, Application US/09626939
;  GENERAL INFORMATION:
;    APPLICANT:  SAMSON, MICHEL
;    APPLICANT:  PARMENTIER, MARC
;    APPLICANT:  VASSART, GILBERT
;    APPLICANT:  LIBERT, FREDERICK
;    TITLE OF INVENTION:  ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;    TITLE OF INVENTION:  AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/626,939
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/833,752
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  184 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-626-939-4

  Query Match             85.4%;  Score 958;  DB 20;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 9
US-09-938-703-4
; Sequence 4, Application US/09938703
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/938,703
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 2000-07-27
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 184 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

  Query Match             85.4%;  Score 958;  DB 23;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 10
US-09-938-719-4
; Sequence 4, Application US/09938719
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear
;             STREET: 620 Newport Center Drive  16th Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/938,719
;             FILING DATE: 24-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/626,939
;             FILING DATE: 27-JULY-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Altman, Daniel E
;             REGISTRATION NUMBER: 34,115
;             REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 184 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4

  Query Match             85.4%;  Score 958;  DB 23;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 11
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US-09-939-226-4
; Sequence 4, Application US/09939226
;  GENERAL INFORMATION:
;       APPLICANT: SAMSON, MICHEL
;                  PARMENTIER, MARC
;                  VASSART, GILBERT
;                  LIBERT, FREDERICK
;       TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                           AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive  16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/939,226
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/626,939
;            FILING DATE: 2000-07-27
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Altman, Daniel E
;            REGISTRATION NUMBER: 34,115
;            REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 184 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4

  Query Match            85.4%;  Score 958;  DB 23;  Length 184;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 12
PCT-US01-04152A-22
; Sequence 22, Application PC/TUS0104152A
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Roschke, Victor
;  APPLICANT:  Li, Yi
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115PC0B
;  CURRENT APPLICATION NUMBER: PCT/US01/04152A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,258
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 60/187,999
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: US 60/234,336
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US01-04152A-22

  Query Match            85.4%;  Score 958;  DB 1;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 13
PCT-US01-04153A-22
; Sequence 22, Application PC/TUS0104153A
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Roschke, Viktor
;  APPLICANT:  Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115PC0D
;  CURRENT APPLICATION NUMBER: PCT/US01/04153A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,258
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 60/187,999
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: US 60/234,336
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US01-04153A-22

  Query Match            85.4%;  Score 958;  DB 1;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 14
PCT-US01-06699-1
; Sequence 1, Application PC/TUS0106699
; GENERAL INFORMATION:
;  APPLICANT:  Progenics Pharmaceuticals,  Inc., et  al.
;  TITLE OF INVENTION:   SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE:   2048/61010-A-PCT/JPW/SHS/AX
;  CURRENT APPLICATION NUMBER: PCT/US01/06699
;  CURRENT FILING DATE:  2001-02-28
;  NUMBER OF SEQ ID NOS:   17
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: human
PCT-US01-06699-1

  Query Match             85.4%;  Score 958;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
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Db        181 HFPY 184


RESULT 15
PCT-US01-10708-3
; Sequence 3, Application PC/TUS0110708
; GENERAL INFORMATION:
;  APPLICANT: Genaissance Pharmaceuticals Inc.
;  APPLICANT:  Choi, Julie
;  APPLICANT:  Klicm, Stefanie E.
;  APPLICANT:  Koshy, Beena
;  TITLE OF INVENTION: Haplotypes of the CCR5 Gene
;  FILE REFERENCE: MWH-0505CT CCR5
;  CURRENT APPLICATION NUMBER: PCT/US01/10708
;  CURRENT FILING DATE:  2001-04-04
;  PRIOR APPLICATION NUMBER: 60/194,361
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapien
PCT-US01-10708-3

  Query Match             85.4%;  Score 958;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-87;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


Search completed: June  3, 2003, 15:31:05
Job time : 171.635 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:19:46 ; Search time 47.7778 Seconds
(without alignments)
947.732 Million cell updates/sec

Title: US-09-939-226-6
Perfect score: 1122
Sequence: 1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASVSK 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1005926 seqs, 210607049 residues

Total number of hits satisfying chosen parameters: 1005926

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
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5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	958	85.4	352	1	PCT-US02-29560-259	Sequence 259, App
2	958	85.4	352	1	PCT-US02-06345-1	Sequence 1, Appli
3	958	85.4	352	1	PCT-US03-03763-1	Sequence 1, Appli
4	958	85.4	352	5	US-09-949-002-303	Sequence 303, App
5	958	85.4	352	5	US-09-949-004-242	Sequence 242, App
6	958	85.4	352	6	US-10-086-814-1	Sequence 1, Appli
7	958	85.4	352	6	US-10-245-882-259	Sequence 259, App
8	958	85.4	352	6	US-10-323-314-1	Sequence 1, Appli
9	958	85.4	352	6	US-10-225-567A-352	Sequence 352, App
10	958	85.4	352	6	US-10-290-058A-6	Sequence 6, Appli
11	958	85.4	352	6	US-10-360-828-1	Sequence 1, Appli
12	958	85.4	352	6	US-10-239-423-67	Sequence 67, Appl
13	958	85.4	352	7	US-60-452-680-12568	Sequence 12568, A
14	958	85.4	352	7	US-60-453-135-7850	Sequence 7850, Ap
15	958	85.4	352	7	US-60-453-050-7850	Sequence 7850, Ap
16	958	85.4	352	7	US-60-455-444-4380	Sequence 4380, Ap
17	958	85.4	352	7	US-60-465-241-4380	Sequence 4380, Ap
18	958	85.4	352	7	US-60-466-412-7850	Sequence 7850, Ap
19	958	85.4	378	5	US-09-949-002-552	Sequence 552, App
20	958	85.4	378	5	US-09-949-004-442	Sequence 442, App
21	839	74.8	332	6	US-10-095-876A-2	Sequence 2, Appli
22	775	69.1	354	6	US-10-219-051B-10290	Sequence 10290, A
23	775	69.1	354	6	US-10-219-051B-10294	Sequence 10294, A
24	766	68.3	268	6	US-10-160-619-164	Sequence 164, App
25	762	67.9	268	6	US-10-160-619-162	Sequence 162, App
26	694	61.9	360	6	US-10-225-567A-460	Sequence 460, App
27	694	61.9	360	6	US-10-239-423-64	Sequence 64, Appl
28	694	61.9	360	7	US-60-452-680-12372	Sequence 12372, A
29	694	61.9	360	7	US-60-453-135-7700	Sequence 7700, Ap
30	694	61.9	360	7	US-60-453-050-7700	Sequence 7700, Ap
31	694	61.9	360	7	US-60-455-444-4289	Sequence 4289, Ap
32	694	61.9	360	7	US-60-465-241-4289	Sequence 4289, Ap
33	694	61.9	360	7	US-60-466-412-7700	Sequence 7700, Ap
34	694	61.9	374	5	US-09-949-004-244	Sequence 244, App
35	694	61.9	374	5	US-09-893-512A-13	Sequence 13, Appl
36	694	61.9	374	6	US-10-239-423-63	Sequence 63, Appl
37	694	61.9	374	6	US-10-219-051B-10292	Sequence 10292, A
38	694	61.9	374	6	US-10-219-051B-10296	Sequence 10296, A
39	694	61.9	374	7	US-60-452-680-12373	Sequence 12373, A
40	694	61.9	374	7	US-60-453-135-7701	Sequence 7701, Ap
41	694	61.9	374	7	US-60-453-050-7701	Sequence 7701, Ap
42	694	61.9	374	7	US-60-455-444-4290	Sequence 4290, Ap
43	694	61.9	374	7	US-60-465-241-4290	Sequence 4290, Ap
44	694	61.9	374	7	US-60-466-412-7701	Sequence 7701, Ap
45	694	61.9	377	5	US-09-949-004-443	Sequence 443, App

ALIGNMENTS

RESULT 1
PCT-US02-29560-259
; Sequence 259, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; CURRENT FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 259
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560-259

Query Match 85.4%; Score 958; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
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RESULT 2

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PCT-US02-06345-1
; Sequence 1, Application PC/TUS0206345
; GENERAL INFORMATION:
;  APPLICANT: Progenics Pharmaceuticals, Inc., et al.
;  TITLE OF INVENTION: Sulfated CCR5 Peptides For HIV-1 Infection
;  FILE REFERENCE: 61010-AB1-PCT/JPW/JTL
;  CURRENT APPLICATION NUMBER: PCT/US02/06345
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
PCT-US02-06345-1

  Query Match             85.4%;  Score 958;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 3
PCT-US03-03763-1
; Sequence 1, Application PC/TUS0303763
; GENERAL INFORMATION:
;  APPLICANT: Hua, Shaobing
;  APPLICANT:  Pauling, Michelle H.
;  APPLICANT:  Zhu, Li
;  TITLE OF INVENTION: METHODS FOR GENERATING ANTIBODIES AGAINST MEMBRANE PROTEINS
;  FILE REFERENCE: 25636-728
;  CURRENT APPLICATION NUMBER: PCT/US03/03763
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 10/071,866
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 10/072,301
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 10/133,978
;  PRIOR FILING DATE: 2002-04-25
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US03-03763-1

  Query Match             85.4%;  Score 958;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 4
US-09-949-002-303
; Sequence 303, Application US/09949002
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 303
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-002-303

  Query Match             85.4%;  Score 958;  DB 5;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 5
US-09-949-004-242
; Sequence 242, Application US/09949004
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000848
;  CURRENT APPLICATION NUMBER: US/09/949,004
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: 60/232,045
;  PRIOR FILING DATE: 2000-09-13
;  NUMBER OF SEQ ID NOS: 6961
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 242
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-004-242
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  Query Match           85.4%;  Score 958;  DB 5;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 6
US-10-086-814-1
; Sequence 1, Application US/10086814
; GENERAL INFORMATION:
;  APPLICANT: Dragic, Tatjana
;  APPLICANT:  Olson, William C.
;  TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE: 61010-AB-1
;  CURRENT APPLICATION NUMBER: US/10/086,814
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-086-814-1

  Query Match           85.4%;  Score 958;  DB 6;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 7
US-10-245-882-259
; Sequence 259, Application US/10245882
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Wilson, Keith E.
;  APPLICANT:  Zlotnik, Albert
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-002710US
;  CURRENT APPLICATION NUMBER: US/10/245,882
;  CURRENT FILING DATE:  2002-12-13
;  PRIOR APPLICATION NUMBER: US 60/323,469
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/323,887
;  PRIOR FILING DATE: 2001-09-20
;  PRIOR APPLICATION NUMBER: US 60/325,114
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/340,944
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/355,145
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/355,257
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/369,899
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 412
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 259
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-245-882-259

  Query Match           85.4%;  Score 958;  DB 6;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 8
US-10-323-314-1
; Sequence 1, Application US/10323314
; GENERAL INFORMATION:
;  APPLICANT: Dragic, Tatjana
;  APPLICANT:  Olson, William
;  TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;  FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
;  CURRENT APPLICATION NUMBER: US/10/323,314
;  CURRENT FILING DATE:  2002-12-19
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: human
US-10-323-314-1

  Query Match           85.4%;  Score 958;  DB 6;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

RESULT 9
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match 85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

RESULT 10
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
; FILE REFERENCE: MPI01-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match 85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

RESULT 11
US-10-360-828-1
; Sequence 1, Application US/10360828
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-360-828-1

Query Match 85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

```
RESULT 12
US-10-239-423-67
; Sequence 67, Application US/10239423
; GENERAL INFORMATION:
;  APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
;  APPLICANT:  HEITLAND, Aleksandra; SPODSBERG, Nikolaj
;  TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
;  TITLE OF INVENTION:  Cell Surface Proteome of Tumor and Inflammation Cells and
;  TITLE OF INVENTION:  for Treating Tumor Diseases and Inflammatory Diseases,
;  TITLE OF INVENTION:  Preferably with the Aid of Specific Chemokine
;  TITLE OF INVENTION:  Receptor Analysis and Chemokine Receptor/Ligand Interaction
;  FILE REFERENCE: 022217us
;  CURRENT APPLICATION NUMBER: US/10/239,423
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: DE10016013.1
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67

  Query Match             85.4%;  Score 958;  DB 6;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 13
US-60-452-680-12568
; Sequence 12568, Application US/60452680
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  GRUPE, Andrew
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001450
;  CURRENT APPLICATION NUMBER: US/60/452,680
;  CURRENT FILING DATE:  2003-03-07
;  NUMBER OF SEQ ID NOS: 116213
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12568
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-452-680-12568

  Query Match             85.4%;  Score 958;  DB 7;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 14
US-60-453-135-7850
; Sequence 7850, Application US/60453135
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001456
;  CURRENT APPLICATION NUMBER: US/60/453,135
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7850
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-135-7850

  Query Match             85.4%;  Score 958;  DB 7;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184


RESULT 15
US-60-453-050-7850
; Sequence 7850, Application US/60453050
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  LUKE, May
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001457
;  CURRENT APPLICATION NUMBER: US/60/453,050
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7850
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-60-453-050-7850

Query Match 85.4%; Score 958; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Qy         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

Qy        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180

Qy        181 HFPY 184
              ||||
Db        181 HFPY 184
```

Search completed: June 3, 2003, 15:33:14
Job time : 47.7778 secs